

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 22, 2005, 20:39:17 ; Search time 42 Seconds
(without alignments)
31.992 Million cell updates/sec

Title: US-10-721-839-32

Sequence: 1 GICRCICTRGRCICGR 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCUTS_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105	91.3	18	US-10-141-645-6	Sequence 6, Appl1
2	102	88.7	18	US-10-141-645-1	Sequence 1, Appl1
3	99	86.1	18	US-10-141-645-2	Sequence 2, Appl1
4	97	84.3	18	US-10-141-645-3	Sequence 3, Appl1
5	97	84.3	18	US-10-141-645-4	Sequence 4, Appl1
6	97	84.3	18	US-10-141-645-5	Sequence 5, Appl1
7	95	82.6	18	US-10-141-645-7	Sequence 7, Appl1
8	88	76.5	18	US-09-309-487-1	Sequence 1, Appl1
9	88	76.5	18	US-09-309-487-8	Sequence 8, Appl1
10	87	75.7	18	US-10-141-645-8	Sequence 9, Appl1
11	87	75.7	18	US-10-141-645-9	Sequence 9, Appl1
12	86	74.8	18	US-09-917-340-53	Sequence 53, Appl1
13	85	73.9	18	US-09-309-487-9	Sequence 9, Appl1
14	85	73.9	18	US-09-309-487-9	Sequence 9, Appl1
15	73	63.5	92	US-09-309-487-21	Sequence 21, Appl1
16	73	63.5	92	US-09-309-487-21	Sequence 21, Appl1
17	64	55.7	76	US-09-309-487-14	Sequence 14, Appl1
18	64	55.7	76	US-09-309-487-29	Sequence 29, Appl1
19	64	55.7	76	US-09-309-487-29	Sequence 29, Appl1
20	64	55.7	76	US-09-309-487-29	Sequence 29, Appl1
21	64	55.7	76	US-09-309-487-29	Sequence 29, Appl1
22	61	53.0	180	US-10-141-645-15	Sequence 15, Appl1
23	61	53.0	2732	US-09-086-436-30	Sequence 286, App
24	58	50.4	9	US-09-309-487-18	Sequence 30, Appl1
25	58	50.4	9	US-09-309-487-18	Sequence 18, Appl1
26	58	50.4	9	US-09-309-487-18	Sequence 18, Appl1
27	56	48.7	9	US-10-141-645-36	Sequence 36, Appl1
			4	US-10-141-645-49	Sequence 49, Appl1

28	55.5	48.3	2211	3	US-09-738-884-1	Sequence 1, Appl1
29	55.5	48.3	2211	4	US-10-096-961A-1	Sequence 1, Appl1
30	55	47.8	1417	3	US-08-900-230-3	Sequence 3, Appl1
31	54	47.0	14	2	US-08-685-589A-157	Sequence 157, App
32	54	47.0	70	3	US-09-188-930-131	Sequence 131, App
33	54	47.0	70	4	US-09-312-283C-131	Sequence 131, App
34	54	47.0	168	4	US-09-252-991A-32502	Sequence 32502, A
35	53	46.1	14	2	US-08-685-589A-156	Sequence 156, App
36	53	46.1	14	2	US-08-685-589A-159	Sequence 159, App
37	53	46.1	18	3	US-09-604-864-8	Sequence 8, Appl1
38	53	46.1	18	3	US-09-604-864-9	Sequence 9, Appl1
39	53	46.1	18	4	US-10-042-872-8	Sequence 8, Appl1
40	53	46.1	18	4	US-10-042-872-9	Sequence 9, Appl1
41	52.5	45.7	1345	2	US-08-977-767-3	Sequence 3, Appl1
42	52	45.2	9	4	US-10-141-645-22	Sequence 22, Appl1
43	52	45.2	9	4	US-10-141-645-34	Sequence 34, Appl1
44	52	45.2	1652	4	US-09-627-650B-1	Sequence 1, Appl1
45	52	45.2	1652	4	US-09-436-063C-1	Sequence 1, Appl1

ALIGNMENTS

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RESULT 1
US-10-141-645-6
; Sequence 6, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Marling
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: US/10/141,645
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic variant
US-10-141-645-6

Query Match          91.3%; Score 105; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.2e-06;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy      1  GICRCICTRGRCICGR 18
Db      1  GICRCICGRGRCICGR 18

RESULT 2
US-10-141-645-1
; Sequence 1, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Marling
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: US/10/141,645
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; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-141-645-1
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Query Match      88.7%; Score 102; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.2e-06;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy      1 GICRCITRGFCRCICGR 18
Db      1 GICRCICGRCICRCICGR 18
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RESULT 3
US-10-141-645-2
; Sequence 2, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; TITLE OF INVENTION: Antimicrobial Peptides
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: US/10/141,645
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic variant
; US-10-141-645-2
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Query Match      86.1%; Score 99; DB 4; Length 18;
Best Local Similarity 83.3%; Pred. No. 2e-05;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy      1 GICRCITRGFCRCICGR 18
Db      1 GICRCICGRCICRCICGR 18
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RESULT 4
US-10-141-645-3
; Sequence 3, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; TITLE OF INVENTION: Antimicrobial Peptides
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: US/10/141,645
; CURRENT FILING DATE: 2002-05-06
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; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic variant
; US-10-141-645-3
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Query Match      84.3%; Score 97; DB 4; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.4e-05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy      1 GICRCITRGFCRCICGR 18
Db      1 GICRCICGRCICRCICGR 18
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RESULT 5
US-10-141-645-4
; Sequence 4, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; TITLE OF INVENTION: Antimicrobial Peptides
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: US/10/141,645
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic variant
; US-10-141-645-4
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Query Match      84.3%; Score 97; DB 4; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.4e-05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
Qy      1 GICRCITRGFCRCICGR 18
Db      1 GICRCICGRCICRCICGR 18
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```

RESULT 6
US-10-141-645-5
; Sequence 5, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; TITLE OF INVENTION: Antimicrobial Peptides
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: US/10/141,645
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; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic variant
US-10-141-645-5
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Query Match      84.3%; Score 97; DB 4; Length 18;
Best Local Similarity 83.3%; Pred. No. 3,4e-05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY      1 GICRCICTRGFCRCICGR 18
DB      1 GYCRCICGRCICRCICGR 18
```

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RESULT 7
US-10-141-645-7
; Sequence 7, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; TITLE OF INVENTION: Antimicrobial Peptides
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: US/10/141,645
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic variant
US-10-141-645-7
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Query Match      82.6%; Score 95; DB 4; Length 18;
Best Local Similarity 83.3%; Pred. No. 5,7e-05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY      1 GICRCICTRGFCRCICGR 18
DB      1 GICRCICGRCICRCICGR 18
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RESULT 8
US-09-309-487-1
; Sequence 1, Application US/09309487
; Patent No. 6335318
; GENERAL INFORMATION:
; APPLICANT: Seisted, Michael E.
; APPLICANT: Tang, Yi-Quan
; APPLICANT: Yuan, Jun
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
; FILE REFERENCE: P-UC 3095
; CURRENT APPLICATION NUMBER: US/09/309,487
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; CURRENT FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-309-487-1
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Query Match      76.5%; Score 88; DB 3; Length 18;
Best Local Similarity 72.2%; Pred. No. 0.00036;
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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QY      1 GICRCICTRGFCRCICGR 18
DB      1 GFCRCICRGVCRCICCTR 18
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RESULT 9
US-09-967-808-1
; Sequence 1, Application US/09967808
; Patent No. 6514727
; GENERAL INFORMATION:
; APPLICANT: Seisted, Michael E.
; APPLICANT: Tang, Yi-Quan
; APPLICANT: Yuan, Jun
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using
; FILE REFERENCE: P-UC 3095
; CURRENT APPLICATION NUMBER: US/09/967,808
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US/09/309,487
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-967-808-1
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Query Match      76.5%; Score 88; DB 4; Length 18;
Best Local Similarity 72.2%; Pred. No. 0.00036;
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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QY      1 GICRCICTRGFCRCICGR 18
DB      1 GFCRCICRGVCRCICCTR 18
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RESULT 10
US-10-141-645-8
; Sequence 8, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; TITLE OF INVENTION: Antimicrobial Peptides
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: US/10/141,645
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 18
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic variant
US-10-141-645-8

Query Match 75.7%; Score 87; DB 4; Length 18;
Best Local Similarity 77.8%; Pred. No. 0.00046;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GICRCICTRGFCRCICGR 18
DB 1 GICICIGYGCRCICGR 18

RESULT 11
US-10-141-645-9
Sequence 9, Application US/10141645
Patent No. 6713078
GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Maring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
FILE REFERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 60/284,855
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: Unassigned
PRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PatscSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic variant
US-10-141-645-9

Query Match 75.7%; Score 87; DB 4; Length 18;
Best Local Similarity 77.8%; Pred. No. 0.00046;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GICRCICTRGFCRCICGR 18
DB 1 GICICIGYGCRCICGR 18

RESULT 12
US-09-917-340-53
Sequence 53, Application US/09917340
Patent No. 6696238
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/290,932
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 53

LENGTH: 18
TYPE: PRT
ORGANISM: Macaca mulatta
US-09-917-340-53

Query Match 74.8%; Score 86; DB 4; Length 18;
Best Local Similarity 86.7%; Pred. No. 0.0006;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RCICTRGFCRCICGR 18
DB 1 RCICTRGFCRCICGR 15

RESULT 13
US-09-309-487-9
Sequence 9, Application US/09309487
Patent No. 6353318
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Tang, Yi-Quan
APPLICANT: Yuan, Jun
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REFERENCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/309,487
CURRENT FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 18
TYPE: PRT
ORGANISM: Macaca mulatta
US-09-309-487-9

Query Match 73.9%; Score 85; DB 3; Length 18;
Best Local Similarity 75.0%; Pred. No. 0.00078;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GICRCICTRGFCRCIC 16
DB 3 GFCRCICRGVCRCIC 18

RESULT 14
US-09-967-808-9
Sequence 9, Application US/09967808
Patent No. 6514727
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Tang, Yi-Quan
APPLICANT: Yuan, Jun
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using
FILE REFERENCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/967,808
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US/09/309,487
PRIOR FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 18
TYPE: PRT
ORGANISM: Macaca mulatta
US-09-967-808-9

Query Match 73.9%; Score 85; DB 4; Length 18;
Best Local Similarity 75.0%; Pred. No. 0.00078;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GICRCICTRGFCRCIC 16

Db 3 GFCRCRCRGVCRCIC 18

RESULT 15
US-09-309-487-21
/ Sequence 21, Application US/09309487
/ Patent No. 6335318
/ GENERAL INFORMATION:
/ APPLICANT: Selsted, Michael E.
/ APPLICANT: Tang, Yi-Quan
/ APPLICANT: Yuen, Jun
/ APPLICANT: Ouellette, Andre J.
/ TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
/ FILE REFERENCE: P-UC 3095
/ CURRENT APPLICATION NUMBER: US/09/309,487
/ CURRENT FILING DATE: 1999-05-10
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 21
/ LENGTH: 92
/ TYPE: PRT
/ ORGANISM: Macaca mulatta
US-09-309-487-21

Query Match 63.5%; Score 73; DB 3; Length 92;
Best Local Similarity 84.6%; Pred. No. 0.064;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 4 RCICTRGFCRCIC 16
Db 65 RCICTRGFCRLC 77

Search completed: March 22, 2005, 20:51:17
Job time : 43 secs

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KM		antibiotic modelling; antimicrobial; cyclic.
XX		unidentified.
OS		
XX		
FH		Location/Qualifiers
FT	Misc-difference	1. .18 /note= "D-form residues"
FT	Misc-difference	1 /note= "Linked to amino acid at position 18 to form a cyclic structure"
FT	Dipeptide-bond	3. .16
FT	Dipeptide-bond	5. .14
FT	Dipeptide-bond	7. .12
FT	Misc-difference	18 /note= "Linked to amino acid at position 1 to form a cyclic structure"
FN		
XX		WO200285401-A1.
PB		31-OCT-2002.
XX		
PF	18-APR-2002;	2002MO-US012353.
PR	18-APR-2001;	2001US-0284855P.
XX		
PA	(REGC)	UNIV CALIFORNIA.
XI	Lehrer RI, Waring AJ, Cole AM, Hong TB,	
DR	WPI; 2003-103387/09.	
XX		
FT	New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually transmitted diseases, vaginosis.	
PS	Disclosure; Page 24; 72pp; English.	
XX		
CC	The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is human retrocyclin peptide analogue	
XX		
SQ	Sequence 18 AA:	
CY	Query Match	86.1%; Score 99; DB 6; Length 18;
ID	Best Local Similarity	83.3%; Pred. No. 0.00089;
Matches	15; Conservative	1; Mismatches 2; Indels 0; Gaps 0;
DB	1 GICRCICTRGFCRICGR 18 1 GICRCICGKIGICRCICGR 18	
RESULT 15		
ID	AAE33802	
XX	AAE33802 standard; peptide; 18 AA.	
AC	AAE33802;	
DT	16-APR-2003 (first entry)	
DE	R9K retrocyclin peptide analogue.	
KW	Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; cyclic.	
OS	Unidentified.	

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XX Key Location/Qualifiers
FH Misc-difference 1 /note= "Linked to amino acid at position 18 to form a
FT cyclic structure"
FT Disulfide-bond 3. .16
FT Disulfide-bond 5. .14
FT Disulfide-bond 7. .12
FT Misc-difference 18
FT /note= "Linked to amino acid at position 1 to form a
FT cyclic structure"
FN WO200285401-A1.
PN
XX 31-OCT-2002.
PD
XX 18-APR-2002; 2002WO-US012353.
PP
XX 18-APR-2001; 2001US-0284855P.
PR
XX (REGC ) UNIV CALIFORNIA.
PA
XX Lehrer RI, Waring AJ, Cole AM, Hong TB;
PI
XX WPI; 2003-103387/09.
DR
XX
XX
XX New isolated retrocyclin peptide, useful for preventing retroviral
XX infections in cells susceptible to bacterial or viral infections or
XX treating patients having the infections, such as HIV, sexually
XX transmitted diseases, vaginosis.
XX
XX Claim 9; Page 24; 72pp; English.
XX
XX The invention relates to novel retrocyclin peptides. Peptides and methods
XX of the invention are useful for preventing retroviral infections in cells
XX susceptible to bacterial or viral infections, or treating patients having
XX infections such as HIV (human immunodeficiency virus), sexually
XX transmitted diseases, bacterial vaginosis or ophthalmic infections. The
XX retrocyclin-mediated killing is useful for modelling and screening novel
XX antibiotics. The invention is also useful in gene therapy. The present
XX sequence is human retrocyclin peptide analogue
XX
XX Sequence 18 AA;
SQ
XX
XX Query Match 86.1%; Score 99; DB 6; Length 18;
XX Best Local Similarity 83.3%; Pred. No. 0.00089;
XX Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0,
XX
XX 1 GICRCICTRGRCICIGR 18
XX ||||| : |||||
XX 1 GICRCICGKICRCICIGR 18

```

XX OS Homo sapiens.
 XX PN WO2004033479-A2.
 XX PD 22-APR-2004.
 XX PF 06-MAY-2003; 2003WO-US014106.
 XX PR 06-MAY-2002; 2002US-00141645.
 XX (REGC) UNIV CALIFORNIA.
 PA (LEHRER/) LEHRER R I.
 PA (WARI/) WARING A J.
 PA (COLE/) COLE A M.
 PA (HONG/) HONG T B.
 XX
 PI Lehrer RI, Waring AJ, Cole AM, Hong TB;
 DR WPI; 2004-340863/31.
 DR N-PSDB; ADN08193.
 XX
 PT New isolated retrocyclin peptides and cyclic polypeptides, useful as
 PT therapeutic and prophylactic agents for treating and preventing microbial
 PT and viral infections.
 PS Claim 9; SEQ ID NO 1; 82pp; English.
 XX
 CC The invention relates to a novel isolated retrocyclin peptide. The
 CC invention further provides: a cyclic polypeptide; an isolated nucleic
 CC acid encoding a primate retrocyclin; a method for preventing retroviral
 CC infection in a cell by administering an effective dose of a circular
 CC minidensin or retrocyclin to the cell; a method for killing microbial
 CC organisms by administering an effective dose of retrocyclin to the
 CC microbial organisms; a method for administering retrocyclin as a
 CC therapeutic agent to a patient with an established microbial or viral
 CC infection; and a method for administering retrocyclin as a prophylactic
 CC agent to prevent a microbial or viral infection in a patient at risk of
 CC developing such infection. The retrocyclin peptide has antibacterial and
 CC virucide activities. The retrocyclin peptide can be used to treat a viral
 CC infection such as HIV-1. The retrocyclin peptide can be used as a vaccine
 CC and can be used in immunotherapy. The peptide and polypeptides are useful
 CC as therapeutic and prophylactic agents for treating and preventing
 CC microbial and viral infections. This sequence represents a retrocyclin
 CC peptide of the invention.
 CC
 SQ Sequence 18 AA;
 Query Match 88.7%; Score 102; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 0.00044;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GICRCICTRGFCRCICGR 18
 DB 1 GICRCICGRGICRCICGR 18
 RESULT 13
 AAB53298
 ID AAB53298 standard; peptide; 18 AA.
 AC AAB53298;
 XX
 DT 13-NOV-2002 (first entry)
 XX
 DE Anti-viral chimeric theta defensin peptide H/RTD-3 SEQ ID NO:31.
 XX
 KW Anti-viral; viral infection; theta-defensin; lipid environment;
 KW amphipathic alpha-helical structure; virucide; anti-HIV; immunisation;
 KW viral growth inhibitor; viral proliferation inhibitor.
 XX
 OS Homo sapiens.
 OS Macaca mulatta.

OS Synthetic.
 XX PN WO200260468-A2.
 XX PD 08-AUG-2002.
 XX PF 29-JAN-2002; 2002WO-US002435.
 XX PR 30-JAN-2001; 2001US-0265270P.
 XX PR 01-JAN-2001; 2001US-0309368P.
 XX (IOWA) UNIV IOWA RES FOUND.
 PA
 PI Maury W, Stapleton J, Stinski M, Roller R, McCreay PB, Tack B;
 DR WPI; 2002-674815/72.
 XX
 PT New method of using a first anti-viral peptide comprising a Theta-
 PT defensin peptide in an amphipathic Alpha-helical structure in a lipid
 PT environment for reducing the infectivity of a virus.
 PS Disclosure; Page 10; 65pp; English.
 XX
 CC The present invention describes a method (M1) of using a first anti-viral
 CC peptide (I) comprising a theta-defensin peptide in an amphipathic alpha
 CC helical structure in a lipid environment for reducing the infectivity of
 CC a virus. (I) can have virucide and anti-HIV activities, and can be used
 CC to reduce virus growth, infectivity burden, shed, and development of anti
 CC -viral resistance. (I) can be used for inhibiting the growth and
 CC proliferation of a virus and so can be used for: (a) protecting or
 CC treating subject from a viral infection, preventing recurrent viral
 CC infection in a subject harbouring a latent virus, controlling viral
 CC spread within a virally-infected subject (VS), reducing viral burden in a
 CC VS, reducing virus shed from a VS, reducing percentage of VS in a
 CC population regardless of viral infection status, or inducing latency in a
 CC VS; (b) reducing the infectivity of a virus; and (c) reducing virus-
 CC contaminated tissue or fluid sample safe for use, or reducing the number
 CC of infectious virus particles in a population of viruses. (M1) is useful
 CC for reducing the infectivity of a virus in sheep, cattle, horses, swine,
 CC cats, fowl and humans e.g. an enveloped virus infecting humans such as
 CC human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is
 CC administered to a patient who is immunosuppressed or to a subject who is
 CC not infected with the virus, where the first anti-viral peptide is
 CC administered prior to or subsequent to the virus contacting the subject.
 CC The anti-viral peptide is most preferably administered to a subject who
 CC is chronically, latently or acutely infected with the virus. The present
 CC sequence represents a chimeric human/rhesus monkey theta defensin anti-
 CC viral peptide, which is given in the exemplification of the present
 CC invention
 CC
 SQ Sequence 18 AA;
 Query Match 87.0%; Score 100; DB 5; Length 18;
 Best Local Similarity 83.3%; Pred. No. 0.00071;
 Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GICRCICTRGFCRCICGR 18
 DB 1 GICRCICRGVCRCICGR 18
 RESULT 14
 AAE33864
 ID AAE33864 standard; peptide; 18 AA.
 AC AAE33864;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE Enantio-RC-101 retrocyclin peptide analogue.
 XX
 KW Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV;
 KW human immunodeficiency virus; bacterial vaginosis; ophthalmic infection;

XX 16-APR-2003 (first entry)
 DT Human retrocyclin peptide.
 XX
 XX Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV;
 KW human immunodeficiency virus; bacterial vaginosis; ophthalmic infection;
 KW antibiotic modelling; antimicrobial; human; cyclic.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 1 /note= "Linked to amino acid at position 18 to form a
 FT cyclic structure"
 FT Disulfide-bond 3..16
 FT Disulfide-bond 5..14
 FT Disulfide-bond 7..12
 FT Misc-difference 18 /note= "Linked to amino acid at position 1 to form a
 FT cyclic structure"
 FT
 XX WO200285401-A1.
 PN
 XX 31-OCT-2002.
 PD
 XX 18-APR-2002; 2002WO-US012353.
 XX
 XX 18-APR-2001; 2001US-0284855P.
 XX
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX
 XX PI Lehrer RI, Waring AJ, Cole AM, Hong TB;
 DR WPI; 2003-103387/09.
 XX
 XX New isolated retrocyclin peptide, useful for preventing retroviral
 PT infections in cells susceptible to bacterial or viral infections or
 PT treating patients having the infections, such as HIV, sexually
 PT transmitted diseases, vaginosis.
 PT
 XX
 XX Claim 9; Page 24; 72pp; English.
 PS
 XX The invention relates to novel retrocyclin peptides. Peptides and methods
 CC of the invention are useful for preventing retroviral infections in cells
 CC susceptible to bacterial or viral infections, or treating patients having
 CC infections such as HIV (human immunodeficiency virus), sexually
 CC transmitted diseases, bacterial vaginosis or ophthalmic infections. The
 CC retrocyclin-mediated killing is useful for modelling and screening novel
 CC antibiotics. The invention is also useful in gene therapy. The present
 CC sequence is human retrocyclin peptide
 CC
 XX Sequence 18 AA;
 SQ
 XX
 XX Query Match 88.7%; Score 102; DB 6; Length 18;
 XX Best Local Similarity 88.9%; Pred. No. 0.00044;
 XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GICRCICTRGFCRCICGR 18
 DB 1 GICRCICGRCICRCICGR 18
 XX
 XX RESULT 11
 XX AAE33863 standard; peptide; 18 AA.
 ID AAE33863
 XX
 XX AAE33863;
 AC
 XX 16-APR-2003 (first entry)
 DT
 XX Enantio-retrocyclin peptide analogue.
 DE
 XX

KW Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV;
 KW human immunodeficiency virus; bacterial vaginosis; ophthalmic infection;
 KW antibiotic modelling; antimicrobial; cyclic.
 XX
 XX Unidentified.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 1..18 /note= "D-form residues"
 FT
 FT Misc-difference 1 /note= "Linked to amino acid at position 18 to form a
 FT cyclic structure"
 FT Disulfide-bond 3..16
 FT Disulfide-bond 5..14
 FT Disulfide-bond 7..12
 FT Misc-difference 18 /note= "Linked to amino acid at position 1 to form a
 FT cyclic structure"
 FT
 XX WO200285401-A1.
 PN
 XX 31-OCT-2002.
 PD
 XX 18-APR-2002; 2002WO-US012353.
 XX
 XX 18-APR-2001; 2001US-0284855P.
 XX
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX
 XX PI Lehrer RI, Waring AJ, Cole AM, Hong TB;
 DR WPI; 2003-103387/09.
 XX
 XX New isolated retrocyclin peptide, useful for preventing retroviral
 PT infections in cells susceptible to bacterial or viral infections or
 PT treating patients having the infections, such as HIV, sexually
 PT transmitted diseases, vaginosis.
 PT
 XX
 XX Disclosure; Page 24; 72pp; English.
 PS
 XX The invention relates to novel retrocyclin peptides. Peptides and methods
 CC of the invention are useful for preventing retroviral infections in cells
 CC susceptible to bacterial or viral infections, or treating patients having
 CC infections such as HIV (human immunodeficiency virus), sexually
 CC transmitted diseases, bacterial vaginosis or ophthalmic infections. The
 CC retrocyclin-mediated killing is useful for modelling and screening novel
 CC antibiotics. The invention is also useful in gene therapy. The present
 CC sequence is human retrocyclin peptide analogue
 CC
 XX Sequence 18 AA;
 SQ
 XX
 XX Query Match 88.7%; Score 102; DB 6; Length 18;
 XX Best Local Similarity 88.9%; Pred. No. 0.00044;
 XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GICRCICTRGFCRCICGR 18
 DB 1 GICRCICGRCICRCICGR 18
 XX
 XX RESULT 12
 XX ADN08176 standard; peptide; 18 AA.
 ID ADN08176
 XX
 XX ADN08176;
 AC
 XX 15-JUL-2004 (first entry)
 DT
 XX Human retrocyclin peptide, RC-100.
 DE
 XX retrocyclin; cyclic; primate; retroviral infection;
 KW circular minidefensin; antibacterial; virucide; vaccine; immunotherapy;
 KW microbial; viral; human.
 KW

KM Monkey; Rhesus theta defensin; RTD-2; antimicrobial peptide; cyclic;
 KM antimicrobial; antiinflammatory; antibacterial; virucide; fungicide;
 KM food; contact lens solution; eye wash solution; inflammatory response;
 KM microbicidal inhibition; microbistatic growth inhibition; disinfectant;
 KM food preservative; bacterial infection; viral infection;
 KM fungal infection; haemolytic activity.
 OS Macaca mulatta.
 XX
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1..18
 FT /note="The peptide is cyclised by a covalent link
 FT between these two residues"
 FT Disulfide-bond 3..16
 FT Disulfide-bond 5..14
 FT Disulfide-bond 7..12
 XX
 XX US2004014669-A1.
 XX
 XX
 XX 22-JAN-2004.
 XX
 XX 30-APR-2003; 2003US-00427715.
 XX
 XX 30-APR-2002; 2002US-0377071P.
 XX
 XX (REGC) UNIV CALIFORNIA.
 XX
 XX Selected ME, Tran DQ;
 XX
 XX WPI; 2004-167945/16.
 XX
 XX
 PT Novel theta defensin analog useful for reducing or inhibiting growth or
 PT survival of a microorganism in an environment such as food or food
 PT product, contact lens solution, or eye wash solution, an inanimate
 PT object.
 XX
 XX Example 1; SEQ ID NO 2; 46pp; English.
 XX
 XX The invention relates to a theta defensin analogue defined by formulae
 CC detailed in the claims or appearing as ADO35239-ADO35257. The theta
 CC defensin analogue is useful for reducing or inhibiting growth or survival
 CC of a microorganism in an environment capable of sustaining the growth or
 CC survival of the microorganism and is useful for reducing or inhibiting
 CC growth or survival of a microorganism in an environment such as food or
 CC food product, a solution (e.g., contact lens solution, or eye wash
 CC solution), an inanimate object comprising surface, or a mammal. The
 CC peptides are also useful for decreasing inflammatory response and for
 CC microbicidal inhibition of survival of microorganism as well as
 CC microbistatic inhibition of growth. Thus the peptides are useful as
 CC therapeutic agents, disinfectants, food preservatives, or medicaments.
 CC The peptides are also useful for treating a patient suffering from
 CC bacterial, viral, fungal or other infection. The theta defensins have
 CC high antimicrobial activity and low haemolytic activity. The present
 CC sequence represents the rhesus monkey wild-type theta defensin RTD-2.
 CC
 XX
 XX Sequence 18 AA;
 SQ
 Query Match 89.6%; Score 103; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 0.00055;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GICRCICTRGFCRCICGR 18
 DB 1 GICRCICTRGFCRCICGR 18
 RESULT 9
 ABP53294
 ID ABP53294 standard; peptide; 18 AA.
 XX
 AC ABP53294;
 XX
 DT 13-NOV-2002 (first entry)

XX
 XX Synthetic anti-viral human theta defensin peptide RTD-1 SEQ ID NO:27.
 DE
 XX Anti-viral; viral infection; theta-defensin; lipid environment;
 KM amphipathic alpha-helical structure; virucide; anti-HIV; immunisation;
 KM viral growth inhibitor; viral proliferation inhibitor.
 XX
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX
 XX MO200260468-A2.
 XX
 XX 08-AUG-2002.
 XX
 XX 29-JAN-2002; 2002WO-US002435.
 XX
 XX 30-JAN-2001; 2001US-0265270P.
 XX
 XX 01-AUG-2001; 2001US-0309368P.
 XX
 XX (IOWA) UNIV IOWA RES FOUND.
 XX
 XX Maury W, Stapleton J, Stinski M, Roller R, McCreary PB, Tack B;
 XX WPI; 2002-674815/72.
 XX
 XX
 PT New method of using a first anti-viral peptide comprising a Theta-
 PT defensin peptide in an amphipathic Alpha-helical structure in a lipid
 PT environment for reducing the infectivity of a virus.
 XX
 XX Disclosure; Page 9; 65pp; English.
 XX
 XX The present invention describes a method (M1) of using a first anti-viral
 CC peptide (I) comprising a theta-defensin peptide in an amphipathic alpha-
 CC helical structure in a lipid environment for reducing the infectivity of
 CC a virus. (I) can have virucide and anti-HIV activities, and can be used
 CC to reduce virus growth, infectivity burden, shed, and development of anti-
 CC -viral resistance. (I) can be used for inhibiting the growth and
 CC proliferation of a virus and so can be used for: (a) protecting or
 CC treating subject from a viral infection, preventing recurrent viral
 CC infection in a subject harbouring a latent virus, controlling virus
 CC spread within a virally-infected subject (VS), reducing viral burden in a
 CC VS, reducing virus shed from a VS, reducing percentage of VS in a
 CC population regardless of viral infection status, or inducing latency in a
 CC VS; (b) reducing the infectivity of a virus; and (c) rendering virus-
 CC contaminated tissue or fluid sample safe for use, or reducing the number
 CC of infectious virus particles in a population of viruses. (M1) is useful
 CC for reducing the infectivity of a virus in sheep, cattle, horses, swine,
 CC cats, fowl and humans e.g. an enveloped virus infecting humans such as
 CC human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is
 CC administered to a patient who is immunosuppressed or to a subject who is
 CC not infected with the virus, where the first anti-viral peptide is
 CC administered prior to or subsequent to the virus contacting the subject.
 CC The anti-viral peptide is most preferably administered to a subject who
 CC is chronically, latently or acutely infected with the virus. The present
 CC sequence represents a human theta defensin anti-viral peptide, which is
 CC given in the exemplification of the present invention
 XX
 XX Sequence 18 AA;
 SQ
 Query Match 88.7%; Score 102; DB 5; Length 18;
 Best Local Similarity 88.9%; Pred. No. 0.00044;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GICRCICTRGFCRCICGR 18
 DB 1 GICRCICTRGFCRCICGR 18
 RESULT 10
 AAE33801
 ID AAE33801 standard; peptide; 18 AA.
 XX
 AC AAE33801;

SQ Sequence 18 AA;

Query Match 90.4%; Score 104; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GICRCICTRGFCRCIC 16
| | | | | | | | | | | | | | | | | |
DB 1 GICRCICTRGFCRCIC 16

RESULT 6

AAB35046
ID AAB35046 standard; peptide; 18 AA.

AC AAB35046;

DT 27-MAR-2001 (first entry)

DE Theta defensin SEQ ID NO: 30.

XX Theta defensin; antimicrobial; cyclic; bacterium; fungus; protozoan;
KW virus; helminth; disinfectant; food preservative; analogue.
XX

OS Unidentified.

PN WO200068265-A1.

PD 16-NOV-2000.

PF 10-MAY-2000; 2000WO-US012842.

PR 10-MAY-1999; 99US-00309487.

PA (REGC) UNIV CALIFORNIA.

PI Selected ME, Tang Y, Yuan J, Quelleter AJ;

DR WPI; 2001-031853/04.

XX Novel theta defensin peptide with antimicrobial activity against
PT bacteria, yeast, fungi, protozoa and viruses.
XX

PS Claim 15; Fig 16; 110pp; English.

CC The present invention provides theta defensin peptides and analogues
CC which have antimicrobial activity. They can be used in the treatment of
CC bacterial, viral, fungal, protozoan and helminthic infections, in
CC disinfectants and as food preservatives
XX

SQ Sequence 18 AA;

Query Match 89.6%; Score 103; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 0.00035;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GICRCICTRGFCRCICR 18
| | | | | | | | | | | | | | | | | |
DB 1 GFCRCICTRGFCRCICR 18

RESULT 7

AAB53295
ID AAB53295 standard; peptide; 18 AA.

AC AAB53295;

DT 13-NOV-2002 (first entry)

DE Anti-viral cheta defensin peptide RTD-2 SEQ ID NO:28.

XX Anti-viral; viral infection; theta-defensin; lipid environment;
KW amphipathic alpha-helical structure; virucide; anti-HIV; immunisation;
XX

KW viral growth inhibitor; viral proliferation inhibitor.

OS Macaca mulatta.
OS Synthetic.
XX

PN WO200260468-A2.

PD 08-AUG-2002.

PF 29-JAN-2002; 2002WO-US002435.

PR 30-JAN-2001; 2001US-0265270P.

PR 01-AUG-2001; 2001US-0309368P.

PA (IOWA) UNIV IOWA RES FOUND.

DR Maury W, Stapleton J, Stinski M, Roller R, McCreary PB, Tack B;

DT WPI; 2002-674815/72.

XX New method of using a first anti-viral peptide comprising a Theta-
PT defensin peptide in an amphipathic Alpha-helical structure in a lipid
PT environment for reducing the infectivity of a virus.
XX

PS Disclosure; Page 10; 65pp; English.

CC The present invention describes a method (M1) of using a first anti-viral
CC peptide (I) comprising a theta-defensin peptide in an amphipathic alpha-
CC helical structure in a lipid environment for reducing the infectivity of
CC a virus. (I) can have virucide and anti-HIV activities, and can be used
CC to reduce virus growth, infectivity burden, shed, and development of anti-
CC viral resistance. (I) can be used for inhibiting the growth and
CC proliferation of a virus and so can be used for: (a) protecting or
CC treating subject from a viral infection, preventing recurrent viral
CC infection in a subject harbouring a latent virus, controlling viral
CC spread within a virally-infected subject (VS), reducing viral burden in a
CC VS, reducing virus shed from a VS, reducing percentage of VS in a
CC population regardless of viral infection status, or inducing latency in a
CC VS; (b) reducing the infectivity of a virus; and (c) rendering virus-
CC contaminated tissue or fluid sample safe for use, or reducing the number
CC of infectious virus particles in a population of viruses. (M1) is useful
CC for reducing the infectivity of a virus in sheep, cattle, horses, swine,
CC cats, fowl and humans e.g. an enveloped virus infecting humans such as
CC human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is
CC administered to a patient who is immunosuppressed or to a subject who is
CC not infected with the virus, where the first anti-viral peptide is
CC administered prior to or subsequent to the virus contacting the subject.
CC The anti-viral peptide is most preferably administered to a subject who
CC is chronically, latently or acutely infected with the virus. The present
CC sequence represents a rhesus monkey cheta defensin anti-viral peptide,
CC which is given in the exemplification of the present invention
XX

SQ Sequence 18 AA;

Query Match 89.6%; Score 103; DB 5; Length 18;
Best Local Similarity 88.9%; Pred. No. 0.00035;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GICRCICTRGFCRCICR 18
| | | | | | | | | | | | | | | | | |
DB 1 GFCRCICTRGFCRCICR 18

RESULT 8

AD035230
ID AD035230 standard; peptide; 18 AA.

AC AD035230;

DT 15-JUL-2004 (first entry)

XX Rhesus cheta defensin peptide, RTD-2.
DE
XX

infection; and a method for administering retrocyclin as a prophylactic agent to prevent a microbial or viral infection in a patient at risk of developing such infection. The retrocyclin peptide has antibacterial and virucide activities. The retrocyclin peptide can be used to treat a viral infection such as HIV-1. The retrocyclin peptide can be used as a vaccine and can be used in immunotherapy. The peptide and polypeptides are useful as therapeutic and prophylactic agents for treating and preventing microbial and viral infections. This sequence represents a retrocyclin peptide of the invention.

Sequence 18 AA;

Query Match 91.3%; Score 105; DB 8; Length 18;
Best Local Similarity 88.9%; Pred. No. 0.00022;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GICRCICRGFCRCICGR 18
Db 1 GICRCICRGFCRCICGR 18

RESULT 4
AAE33866
ID AAE33866 standard; peptide; 18 AA.

AAE33866;
16-APR-2003 (first entry)

Macaca mulatta RTD1 peptide.

Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; rhesus monkey; theta defensin 1A; RTD1.

Macaca mulatta.

WO200285401-A1.

31-OCT-2002.

18-APR-2002; 2002WO-US012353.

18-APR-2001; 2001US-0284855P.

(REGC) UNIV CALIFORNIA.

Lehrer RI, Waring AJ, Cole AM, Hong TB;

WPI; 2003-103387/09.

New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually transmitted diseases, vaginosis.

Example 1; Fig 3C; 72pp; English.

The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is rhesus monkey theta defensin, RTD1 peptide. This sequence is used in the exemplification of the invention

Sequence 18 AA;

Query Match 90.4%; Score 104; DB 6; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.00027;

Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 GICRCICRGFCRCICGR 18
Db 1 GICRCICRGFCRCICGR 18

RESULT 5
ADO35255
ID ADO35255 standard; peptide; 18 AA.

ADO35255;

15-JUL-2004 (first entry)

Rhesus theta defensin analogue peptide RTD-4.

Monkey; Rhesus theta defensin; RTD; antimicrobial peptide; antimicrobial; antiinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; fungal infection; haemolytic activity; cyclic.

Macaca mulatta.
Synthetic.

Key Location/Qualifiers

Modified-site 1..18
/note="The peptide is cyclised by a covalent link between these two residues"

Disulfide-bond 3..16
Disulfide-bond 5..14
Disulfide-bond 7..12

US2004014669-A1.

22-JAN-2004.

30-APR-2003; 2003US-00427715.

30-APR-2002; 2002US-0377071P.

(REGC) UNIV CALIFORNIA.

Selected ME, Tran DQ;

WPI; 2004-167945/16.

Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate object.
Claim 1; SEQ ID NO 29; 46pp; English.

The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO35257. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensin have high antimicrobial activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide.

CC spread within a virally-infected subject (VS), reducing viral burden in a
CC VS, reducing virus shed from a VS, reducing percentage of VS in a
CC population regardless of viral infection status; or inducing latency in a
CC VS; (b) reducing the infectivity of a virus; and (c) rendering virus-
CC contaminated tissue or fluid sample safe for use; or reducing the number
CC of infectious virus particles in a population of viruses. (M) is useful
CC for reducing the infectivity of a virus in sheep, cattle, horses, swine,
CC cats, fowl and humans e.g. an enveloped virus infecting humans such as
CC human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is
CC administered to a patient who is immunosuppressed or to a subject who is
CC not infected with the virus, where the first anti-viral peptide is
CC administered prior to or subsequent to the virus contacting the subject.
CC The anti-viral peptide is most preferably administered to a subject who
CC is chronically, latently or acutely infected with the virus. The present
CC sequence represents a chimeric human/rhesus monkey theta defensin anti-
CC viral peptide, which is given in the exemplification of the present
CC invention

SO Sequence 18 AA;

Query Match 100.0%; Score 115; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GICRCICRGFCRCICGR 18
DB 1 GICRCICRGFCRCICGR 18

RESULT 2
AAE33806
ID AAE33806 standard; peptide; 18 AA.

AC AAE33806;
DT 16-APR-2003 (first entry)

XX 11ly retrocyclin peptide analogue.

DE Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV;
KW human immunodeficiency virus; bacterial vaginosis; ophthalmic infection;
KW antibiotic modelling; antimicrobial; cyclic.

XX Unidentified.

OS Key Location/Qualifiers
FH Misc-difference 1
FT /note= "Linked to amino acid at position 18 to form a
FT cyclic structure"

FT Disulfide-bond 3..16
FT Disulfide-bond 5..14
FT Disulfide-bond 7..12

FT Misc-difference 18
FT /note= "Linked to amino acid at position 1 to form a
FT cyclic structure"

XX WO200285401-A1.

XX 31-OCT-2002.

XX 18-APR-2002; 2002WO-US012353.

XX 18-APR-2001; 2001US-0284855P.

XX (REGC) UNIV CALIFORNIA.

XX PI Lehrer RI, Waring AJ, Cole AM, Hong TB;

XX WPI; 2003-103387/09.

XX New isolated retrocyclin peptide, useful for preventing retroviral
PT infections in cells susceptible to bacterial or viral infections or
PT treating patients having the infections, such as HIV, sexually

PT transmitted diseases, vaginosis.
XX
XX Claim 9; Page 24; 72pp; English.

XX The invention relates to novel retrocyclin peptides. Peptides and methods
CC of the invention are useful for preventing retroviral infections in cells
CC susceptible to bacterial or viral infections, or treating patients having
CC infections such as HIV (human immunodeficiency virus), sexually
CC transmitted diseases, bacterial vaginosis or ophthalmic infections. The
CC retrocyclin-mediated killing is useful for modelling and screening novel
CC antibiotics. The invention is also useful in gene therapy. The present
CC sequence is human retrocyclin peptide analogue

SO Sequence 18 AA;

Query Match 91.3%; Score 105; DB 6; Length 18;
Best Local Similarity 88.9%; Pred. No. 0.00022;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GICRCICRGFCRCICGR 18
DB 1 GICRCICRGFCRCICGR 18

RESULT 3
ADN08181
ID ADN08181 standard; peptide; 18 AA.

AC ADN08181;

DT 15-JUL-2004 (first entry)

XX Human retrocyclin peptide, RC-105.

DE retrocyclin; cyclic; primate; retroviral infection;
KW circular minidensin; antibacterial; virucide; vaccine; immunotherapy;
KW microbial; viral; human.

XX Homo sapiens.
OS Synthetic.

XX WO2004033479-A2.

XX 22-APR-2004.

XX 06-MAY-2003; 2003WO-US014106.

XX 06-MAY-2002; 2002US-00141645.

XX (REGC) UNIV CALIFORNIA.

XX (LEHR/) LEHRER R I.

XX (WARI/) WARING A J.

XX (COLE/) COLE A M.

XX (HONG/) HONG T B.

XX PI Lehrer RI, Waring AJ, Cole AM, Hong TB;

XX WPI; 2004-340883/31.

XX Claim 9; SEQ ID NO 6; 82pp; English.

XX The invention relates to a novel isolated retrocyclin peptide. The
CC invention further provides: a cyclic polypeptide; an isolated nucleic
CC acid encoding a primate retrocyclin; a method for preventing retroviral
CC infection in a cell by administering an effective dose of a circular
CC minidensin or retrocyclin to the cell; a method for killing microbial
CC organisms by administering an effective dose of retrocyclin to the
CC microbial organisms; a method for administering retrocyclin as a
CC therapeutic agent to a patient with an established microbial or viral

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OM protein - protein search, using sw model

Run on: March 22, 2005, 20:22:01 ; Search time 164 Seconds
(without alignments)
42.449 Million cell updates/sec

Title: US-10-721-839-32

Perfect score: 115
Sequence: 1 GICRCITRGFCRCICGR 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp19808:*
- 2: geneseqp19908:*
- 3: geneseqp20008:*
- 4: geneseqp20018:*
- 5: geneseqp20028:*
- 6: geneseqp20038:*
- 7: geneseqp20038:*
- 8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	100.0	18	5	ABP53299 Anti-vira
2	105	91.3	18	6	AAE33806 IL1Y retr
3	105	91.3	18	8	ADN08181 Human ret
4	104	90.4	18	6	AAE33866 Macaca mu
5	104	90.4	18	8	AD035255 Rhesus th
6	103	89.6	18	4	AAE35046 Theta def
7	103	89.6	18	5	ABP53295 Anti-vira
8	103	89.6	18	5	AD035230 Rhesus th
9	102	88.7	18	5	ABP53294 Synthetic
10	102	88.7	18	6	AAE33801 Human ret
11	102	88.7	18	6	AAE33863 Eranthio-r
12	102	88.7	18	8	ADN08176 Human ret
13	100	87.0	18	5	ABP53298 Anti-vira
14	99	86.1	18	6	AAE33864 Aae33864 Eranthio-R
15	99	86.1	18	6	AAE33802 R9K retro
16	99	86.1	18	8	ADN08177 Human ret
17	98	85.2	18	8	AD035240 Rhesus th
18	97	84.3	18	6	AAE33805 IL1Y retr
19	97	84.3	18	6	AAE33804 IL1Y retr
20	97	84.3	18	6	AAE33803 IL1Y retr
21	97	84.3	18	8	ADN08179 Human ret
22	97	84.3	18	8	ADN08180 Human ret
23	97	84.3	18	8	ADN08178 Human ret
24	95	82.6	18	6	AAE33807 R9Y retr
25	95	82.6	18	8	ADN08182 Human ret

26	94	81.7	18	6	AAE33865 RC-101/10
27	93.5	81.3	18	8	AD035263 Monkey RT
28	89	77.4	18	4	AAE35047 Theta def
29	89	77.4	18	5	ABP53296 Anti-vira
30	89	77.4	18	8	AD035231 Rhesus th
31	89	77.4	18	8	AD035242 Rhesus th
32	89	77.4	18	8	AD035241 Rhesus th
33	89	77.4	18	8	AD035241 Rhesus th
34	89	77.4	18	8	AD035256 Rhesus th
35	88	76.5	18	4	AAE35030 Theta def
36	88	76.5	18	5	ABP53297 Anti-vira
37	88	76.5	18	7	AD095202 Cyclic de
38	88	76.5	18	8	AD035357 Antimicro
39	88	76.5	18	8	AD070012 Rhesus th
40	88	76.5	18	8	AD035229 Rhesus th
41	88	76.5	18	8	AD035238 Rhesus th
42	88	76.5	18	8	AD035239 Rhesus th
43	88	76.5	18	8	AD035250 Rhesus th
44	87	75.7	18	6	AAE33809 R13Y retr
45	87	75.7	18	6	AAE33808 R9Y retr

ALIGNMENTS

RESULT 1
ID AAE33299 standard; peptide; 18 AA.
XX AAE33299;
AC AAE33299;
XX 13-NOV-2002 (first entry)
DT Anti-viral chimeric theta defensin peptide H/RTD-2 SEQ ID NO.32.
DE Anti-viral
XX Anti-viral; viral infection; theta-defensin; lipid environment;
XX amphipathic alpha-helical structure; virucide; anti-HIV; immunisation;
KW viral growth inhibitor; viral proliferation inhibitor.
XX Homo sapiens.
OS Macaca mulatta.
OS Synthetic.
XX WO200260468-A2.
XX PN 08-AUG-2002.
XX PD 29-JAN-2002; 2002WO-US002435.
XX PF 30-JAN-2001; 2001US-0265270P.
XX PR 01-AUG-2001; 2001US-0309368P.
XX (IOWA) UNIV IOWA RES FOUND.
PI Maury W, Stapleton J, Stinski M, Roller R, Mccray PB, Tack B;
XX WPI; 2002-674815/72.
XX DR New method of using a first anti-viral peptide comprising a Theta-
XX defensin peptide in an amphipathic Alpha-helical structure in a lipid
XX environment for reducing the infectivity of a virus.
XX PT Disclosure; Page 10; 65pp; English.
XX PS The present invention describes a method (M1) of using a first anti-viral
XX peptide (I1) comprising a theta-defensin peptide in an amphipathic alpha-
XX helical structure in a lipid environment for reducing the infectivity of
XX a virus. (I1) can have virucide and anti-HIV activities, and can be used
XX to reduce virus growth, infectivity burden, shed, and development of anti-
XX viral resistance. (I1) can be used for inhibiting the growth and
XX proliferation of a virus and so can be used for: (a) protecting or
XX treating subject from a viral infection, preventing recurrent viral
XX infection in a subject harbouring a latent virus, controlling virus

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OM protein - protein search, using sw model

Run on: March 22, 2005, 20:46:53 ; Search time 141 Seconds
(without alignments)
42.197 Million cell updates/sec

Title: US-10-721-839-32

Perfect score: 115

Sequence: 1 GICRCICTRGRCICR 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1401741 seqs, 330541175 residues

Total number of hits satisfying chosen parameters: 1401741

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubppa/PCRT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep:*
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- 5: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubppa/PCRTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubppa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubppa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubppa/US09C_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubppa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubppa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubppa/US10D_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubppa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	115	100.0	18	14	US-10-060-102-32
2	115	100.0	18	15	US-10-721-839-32
3	105	91.3	18	14	US-10-141-645-6
4	104	90.4	18	15	US-10-427-715-29
5	103	89.6	18	14	US-10-060-102-28
6	103	89.6	18	15	US-10-427-715-2
7	103	89.6	18	15	US-10-427-715-14
8	103	89.6	18	15	US-10-721-839-28
9	102	88.7	18	14	US-10-060-102-27
10	102	88.7	18	14	US-10-141-645-1
11	102	88.7	18	15	US-10-721-839-27
12	100	87.0	18	14	US-10-060-102-31
13	100	87.0	18	15	US-10-721-839-31

14	99	86.1	18	14	US-10-141-645-2	Sequence 2, Appl1
15	97	84.3	18	14	US-10-141-645-3	Sequence 3, Appl1
16	97	84.3	18	14	US-10-141-645-4	Sequence 4, Appl1
17	97	84.3	18	14	US-10-141-645-5	Sequence 5, Appl1
18	95	82.6	18	14	US-10-141-645-7	Sequence 7, Appl1
19	89	77.4	18	14	US-10-060-102-29	Sequence 29, Appl1
20	89	77.4	18	15	US-10-427-715-3	Sequence 3, Appl1
21	89	77.4	18	15	US-10-427-715-15	Sequence 15, Appl1
22	89	77.4	18	15	US-10-427-715-16	Sequence 16, Appl1
23	89	77.4	18	15	US-10-427-715-30	Sequence 30, Appl1
24	89	77.4	18	15	US-10-721-839-29	Sequence 29, Appl1
25	88	76.5	18	14	US-10-060-102-30	Sequence 30, Appl1
26	88	76.5	18	14	US-10-113-994-1	Sequence 1, Appl1
27	88	76.5	18	15	US-10-427-715-1	Sequence 12, Appl1
28	88	76.5	18	15	US-10-427-715-12	Sequence 13, Appl1
29	88	76.5	18	15	US-10-427-715-13	Sequence 24, Appl1
30	88	76.5	18	15	US-10-427-715-24	Sequence 30, Appl1
31	88	76.5	18	15	US-10-721-839-30	Sequence 8, Appl1
32	87	75.7	18	14	US-10-141-645-8	Sequence 9, Appl1
33	87	75.7	18	14	US-10-141-645-9	Sequence 53, Appl1
34	86	74.8	18	9	US-09-917-340-53	Sequence 17, Appl1
35	86	74.8	18	15	US-10-427-715-17	Sequence 31, Appl1
36	86	74.8	18	15	US-10-427-715-31	Sequence 53, Appl1
37	86	74.8	18	17	US-10-844-837-53	Sequence 9, Appl1
38	85	73.9	18	14	US-10-113-994-9	Sequence 28, Appl1
39	77	67.0	18	15	US-10-427-715-28	Sequence 21, Appl1
40	76	66.1	18	15	US-10-427-715-23	Sequence 51, App
41	73	63.5	92	14	US-10-313-994-21	Sequence 37, Appl
42	72	62.6	101	11	US-09-833-245-511	Sequence 38, Appl
43	71	61.7	18	15	US-10-427-715-38	Sequence 39, Appl
44	71	61.7	18	15	US-10-427-715-38	
45	71	61.7	18	15	US-10-427-715-39	

ALIGNMENTS

RESULT 1

US-10-060-102-32

Sequence 32, Application US/10060102

Publication No. US20030022829A1

GENERAL INFORMATION:

APPLICANT: MAUDRY, WENDY

APPLICANT: STAPLETON, JACK

APPLICANT: ROLLER, RICHARD

APPLICANT: STINSKI, MARK

APPLICANT: MCCRAY, PAUL B.

TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALIA

TITLE OF INVENTION: CATHELICIDINS

FILE REFERENCE: IOWA.035US

CURRENT APPLICATION NUMBER: US/10/060.102

PRIOR FILING DATE: 2002-02-22

PRIOR APPLICATION NUMBER: 60/329,368

PRIOR FILING DATE: 2001-08-01

PRIOR APPLICATION NUMBER: 60/265,270

PRIOR FILING DATE: 2001-01-30

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 32

LENGTH: 18

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Peptide

US-10-060-102-32

Query Match 100.0%; Score 115; DB 14; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.8e-06;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

By 1 GICRCICTRGRCICR 18

Db 1 GICRCICTRGFCRCICGR 18

RESULT 2

US-10-721-839-32
; Sequence 32, Application US/10721839
; Publication No. US20040086535A1
; GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STRAPLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; APPLICANT: TACK, BRIAN
; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI
; FILE REFERENCE: IOWA:035US
; CURRENT APPLICATION NUMBER: US/10/721,839
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: US/10/060,102
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/309,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-721-839-32

Query Match 100.0%; Score 115; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GICRCICTRGFCRCICGR 18
Db 1 GICRCICTRGFCRCICGR 18

RESULT 3

US-10-141-645-6
; Sequence 6, Application US/10141645
; Publication No. US20030144184A1
; GENERAL INFORMATION:
; APPLICANT: Robert Lehnert
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: US/10/141,645
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic variant
US-10-141-645-6

Query Match 91.3%; Score 105; DB 14; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.3e-05;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GICRCICTRGFCRCICGR 18
Db 1 GICRCICGRGYCRCICGR 18

RESULT 4

US-10-427-715-29
; Sequence 29, Application US/10427715
; Publication No. US20040014669A1
; GENERAL INFORMATION:
; APPLICANT: Tran, Dat Q.
; TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
; FILE REFERENCE: Thereof, and Methods of Use
; CURRENT APPLICATION NUMBER: US/10/427,715
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/377,071
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-427-715-29

Query Match 90.4%; Score 104; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GICRCICTRGFCRCIC 16
Db 1 GICRCICTRGFCRCIC 16

RESULT 5

US-10-060-102-28
; Sequence 28, Application US/10060102
; Publication No. US2003002829A1
; GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STRAPLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; APPLICANT: TACK, BRIAN
; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI
; FILE REFERENCE: IOWA:035US
; CURRENT APPLICATION NUMBER: US/10/060,102
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/309,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-060-102-28

Query Match 89.6%; Score 103; DB 14; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.8e-05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GICRCICTRGFCRCICGR 18
DB 1 GFCRCICTRGFCRCICTR 18

RESULT 6

US-10-427-715-2
; Sequence 2, Application US/10427715
; Publication No. US20040014669A1
; GENERAL INFORMATION:
; APPLICANT: Selected, Michael E.
; APPLICANT: Tran, Dat Q.
; TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
; FILE REFERENCE: 66778-302(UC5754)
; CURRENT APPLICATION NUMBER: US/10/427,715
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/377,071
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-10-427-715-2

Query Match 89.6%; Score 103; DB 15; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.8e-05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GICRCICTRGFCRCICGR 18
DB 1 GFCRCICTRGFCRCICTR 18

RESULT 7

US-10-427-715-14
; Sequence 14, Application US/10427715
; Publication No. US20040014669A1
; GENERAL INFORMATION:
; APPLICANT: Selected, Michael E.
; APPLICANT: Tran, Dat Q.
; TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
; FILE REFERENCE: 66778-302(UC5754)
; CURRENT APPLICATION NUMBER: US/10/427,715
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/377,071
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-427-715-14

Query Match 89.6%; Score 103; DB 15; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.8e-05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GICRCICTRGFCRCICGR 18
DB 1 GFCRCICTRGFCRCICTR 18

RESULT 8

US-10-721-839-28
; Sequence 28, Application US/10721839
; Publication No. US20040086535A1
; GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STAPLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; TITLE OF INVENTION: NOVEL ANTI-VIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALIAN
; FILE REFERENCE: IOWA:035US
; CURRENT APPLICATION NUMBER: US/10/721,839
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: US/10/060,102
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/309,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-721-839-28

Query Match 89.6%; Score 103; DB 15; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.8e-05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GICRCICTRGFCRCICGR 18
DB 1 GFCRCICTRGFCRCICTR 18

RESULT 9

US-10-060-102-27
; Sequence 27, Application US/10060102
; Publication No. US20030022829A1
; GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STAPLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; TITLE OF INVENTION: NOVEL ANTI-VIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALIAN
; FILE REFERENCE: IOWA:035US
; CURRENT APPLICATION NUMBER: US/10/060,102
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/309,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-060-102-27

Query Match	88.7%	Score 102;	DB 14;	Length 18;
Best Local Similarity	88.9%	Pred. No. 4.9e-05;		
Matches 16;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy	1	GICRCICTRGFCRCICGR	18
Db	1	GICRCICGRGICRCICGR	18

RESULT 10
US-10-141-645-1

```

1  APPLICANT: Robert Lehner
2  APPLICANT: Alan Maring
3  APPLICANT: Alexander Cole
4  APPLICANT: Teresa Hong
5  TITLE OF INVENTION: Retrocycling - Antiviral and
6  TITLE OF INVENTION: Antimicrobial Peptides
7  FILE REFERENCE: UCLA-00101P
8  CURRENT APPLICATION NUMBER: US/10/141,645
9  CURRENT FILING DATE: 2002-05-06
10 PRIOR APPLICATION NUMBER: 60/284,855
11 PRIOR FILING DATE: 2001-04-18
12 PRIOR APPLICATION NUMBER: Unassigned
13 PRIOR FILING DATE: 2002-04-18
14 NUMBER OF SEQ ID NOS: 125
15 SOFTWARE: PasteSeq for Windows Version 4.0
16 SEQ ID NO: 1
17 LENGTH: 18
18 TYPE: PRT
19 ORGANISM: Homo sapiens
20 OS-10-141-645-1

```

Query Match	88.7%	Score 102;	DB 14;	Length 18;
Best Local Similarity	88.9%	Pred. No. 4.9e-05;		
Matches 16; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Dy

1 GICRCICTRGFCRCICGR 18
||| ||| |
Db

1 GICRCICGRCICRCICGR 18

```

RESULT 11
US-10-721-839-27
; Sequence 27, Application US/10721839
; Publication No. US20040086535a1
; GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STAPLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; APPLICANT: TACK, BRIAN
; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THERA DEFENSINS AND MAMMAL
; TITLE OF INVENTION: CATHELCIDINS
; FILE REFERENCE: IOWA:0350S
; CURRENT APPLICATION NUMBER: US/10/721,839
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: US/10/060,102
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/309,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence

```

```

:   FEATURE:      Description of Artificial Sequence: Synthetic
:   OTHER INFORMATION:
:   OTHER INFORMATION: Peptide
US-10-721-839-27

```

Query Match	88.7%	Score 102	DB 15	Length 18
Best Local Similarity	88.9%	Pred. No.	4.9e-05	
Matches	16	Conservative	0	Mismatches 2
				Indels 0
				Gaps 0

```
QY      1 GICRCICTRGFCRCICGR 18
        ||||| | |||||
Db      1 GICRCICGRGICRCICGR 18
```

RESULT 12
US-10-060-102-31

```

Publication No.: US20030022829A1
GENERAL INFORMATION:
APPLICANT: MAURI, WENDY
APPLICANT: STAPLETON, JACK
APPLICANT: ROLLER, RICHARD
APPLICANT: STINSKI, MARK
APPLICANT: MCCRAY, PAUL B.
APPLICANT: TACK, BRIAN
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALIAN
TITLE OF INVENTION: CATHELICIDINS
FILE REFERENCE: IOWA:03US
CURRENT APPLICATION NUMBER: US/10/060,102
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 60/309,368
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/265,270
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1

```

```

; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence

```

```

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-060-102-31

```

Query Match	87.0%	Score 100; DB 14	Length 18;
Best Local Similarity	83.3%	Pred. No. 8.2e-05;	
Matches 15; Conservative	1;	Mismatches 2;	Indels 0; Gaps 0;

```

QY      1 GICRCICTRGFCRCICGR 18
         |||||:| || |||||
Db      1 GICRCLCRGVCRCICGR 18

```

RESULT 13
 US-10-721-839-31
 ; Sequence 31, Application US/10721839
 ; Publication No. US20040086535A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MAURY, WENDY
 ; APPLICANT: STAPLETON, JACK
 ; APPLICANT: ROLLER, RICHARD
 ; APPLICANT: STINSKI, MARK
 ; APPLICANT: MCCRAY, PAUL B.
 ; APPLICANT: TACK, BRIAN
 ; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIVATE THETA DEFENSINS AND MAMMALIIDS
 ; TITLE OF INVENTION: CATHELICIDINS
 ; FILE REFERENCE: IOWA:035US
 ; CURRENT APPLICATION NUMBER: US/10/721, 839
 ; CURRENT FILING DATE: 2003-11-25
 ; PRIOR APPLICATION NUMBER: US/10/060,102
 ; PRIOR FILING DATE: 2002-02-22
 ; PRIOR APPLICATION NUMBER: 60/309,368
 ;

;; PRIOR FILING DATE: 2001-08-01
;; PRIOR APPLICATION NUMBER: 60/265,270
;; PRIOR FILING DATE: 2001-01-30
;; NUMBER OF SEQ ID NOS: 32
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 31
;; LENGTH: 18
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: Peptide
US-10-721-839-31

Query Match 87.0%; Score 100; DB 15; Length 18;
Best Local Similarity 83.3%; Pred. No. 8.2e-05;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GICRCICTRGFCRCICGR 18
|||:|||||
Db 1 GICRCLCRGVCRCICGR 18

RESULT 14
US-10-141-645-2
;; Sequence 2, Application US/10141645
;; Publication No. US20030144184A1
;; GENERAL INFORMATION:
;; APPLICANT: Robert Lehrer
;; APPLICANT: Alan Waring
;; APPLICANT: Alexander Cole
;; APPLICANT: Teresa Hong
;; TITLE OF INVENTION: Retrocyclins - Antiviral and
;; TITLE OF INVENTION: Antimicrobial Peptides
;; FILE REFERENCE: UCLA-001CIP
;; CURRENT APPLICATION NUMBER: US/10/141,645
;; PRIOR FILING DATE: 2002-05-06
;; PRIOR APPLICATION NUMBER: 60/284,855
;; PRIOR FILING DATE: 2001-04-18
;; PRIOR APPLICATION NUMBER: Unassigned
;; PRIOR FILING DATE: 2002-04-18
;; NUMBER OF SEQ ID NOS: 125
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 18
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: synthetic variant
US-10-141-645-2

Query Match 86.1%; Score 99; DB 14; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.00011;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GICRCICTRGFCRCICGR 18
|||:|||||
Db 1 GICRCICGKICRCICGR 18

RESULT 15
US-10-141-645-3
;; Sequence 3, Application US/10141645
;; Publication No. US20030144184A1
;; GENERAL INFORMATION:
;; APPLICANT: Robert Lehrer
;; APPLICANT: Alan Waring
;; APPLICANT: Alexander Cole
;; APPLICANT: Teresa Hong
;; TITLE OF INVENTION: Retrocyclins - Antiviral and
;; TITLE OF INVENTION: Antimicrobial Peptides
;; FILE REFERENCE: UCLA-001CIP
;; CURRENT APPLICATION NUMBER: US/10/141,645

;; CURRENT FILING DATE: 2002-05-06
;; PRIOR APPLICATION NUMBER: 60/284,855
;; PRIOR FILING DATE: 2001-04-18
;; PRIOR APPLICATION NUMBER: Unassigned
;; PRIOR FILING DATE: 2002-04-18
;; NUMBER OF SEQ ID NOS: 125
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 18
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: synthetic variant
US-10-141-645-3

Query Match 84.3%; Score 97; DB 14; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.00018;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GICRCICTRGFCRCICGR 18
|||:|||||
Db 1 GICRCYCGKICRCICGR 18

Search completed: March 22, 2005, 21:02:08
Job time : 144 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 22, 2005, 20:37:47 ; Search time 39 Seconds
(without alignments)
44,408 Million cell updates/sec

Title: US-10-721-839-32
Perfect score: 115
Sequence: 1 GICRCICTRGFCRCICGR 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR 79: *
2: PIR: *
3: PIR: *
4: PIR: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	74.8	18	2	CS9089
2	64	55.7	76	2	AS9089
3	57.5	50.0	248	2	E71602
4	51	44.3	164	2	T24272
5	51	44.3	188	2	T15651
6	51	44.3	306	2	S32834
7	50.5	43.9	3461	2	S58870
8	49.5	43.0	282	2	UC5677
9	49	42.6	72	1	T1MB
10	49	42.6	73	2	UC1066
11	49	42.6	1700	2	S08167
12	48	42.6	3191	2	T22945
13	48.5	42.2	83	2	S07405
14	48.5	42.2	94	2	TJ2C25
15	48.5	42.2	103	1	TJ2C25
16	48.5	42.2	419	2	S69207
17	48	42.2	152	2	T18975
18	48	41.7	157	2	A25964
19	48	41.7	624	1	S54581
20	48	41.7	2946	2	T15840
21	47	40.9	72	1	T1ZB1P
22	47	40.9	78	1	T1ZB1P
23	47	40.9	113	2	S56648
24	47	40.9	195	2	T28803
25	47	40.9	290	2	G72858
26	47	40.9	1353	1	JH0675
27	47	40.9	1394	2	A35626
28	47	40.9	1733	1	B45344
29	47	40.9	1958	2	B40505

30	47	40.9	2195	2	T34264	hypothetical prote
31	46.5	40.4	95	2	S02186	hypothetical prote
32	46.5	40.4	143	2	B21761	high cysteine chor
33	46.5	40.4	1131	2	T15617	hypothetical prote
34	46.5	40.4	2871	2	A55567	fibrillin I - bov
35	46.5	40.4	2871	2	A55624	fibrillin-1 precu
36	46.5	40.4	3002	2	A47221	fibrillin-1 precu
37	46	40.0	64	2	A25775	metallothionein A
38	46	40.0	64	2	A33825	metallothionein A
39	46	40.0	79	1	T1P82	proteinase inhibit
40	46	40.0	83	2	S07941	proteinase inhibit
41	46	40.0	102	1	T1SYD2	proteinase inhibit
42	46	40.0	146	2	S09415	proteinase inhibit
43	46	40.0	160	2	T25185	hypothetical prote
44	46	40.0	195	2	JH0719	omega-conotoxin re
45	46	40.0	276	2	F71262	hypothetical prote

ALIGNMENTS

RESULT 1
CS9089
theta defensin-1 - rhesus macaque
N:Alternate names: RFD-1
C:Species: Macaca mulatta (rhesus macaque)
C:Date: 29-Oct-1999 #sequence #revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: CS9089
R:Tang, Y.Q.; Yuan, J.; Osapay, G.; Osapay, K.; Tran, D.; Miller, C.J.; Ouellette, A.J.;
Science 286, 498-502, 1999
A:Title: A cyclic antimicrobial peptide produced in primate leukocytes by the ligation o
A:Reference number: A59089; MUID:99453140; PMID:10521339
A:Accession: CS9089
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <SEL>
A>Note: this sequence is cyclically permuted by -6 residues from the sequence presented
C:Comment: For the two contributing precursor sequences, see PIR:A59089 and PIR:B59089.
C:Keywords: antibacterial; antibiotic; antifungal; leukocyte; protein splicing
F:1-9/Region: theta defensin 1a-derived
F:10-18/Region: theta defensin 1b-derived
F:1-18/Cross-link: cyclopeptide (Arg-Cys) #status experimental
F:2-11,4-9,13-18/Disulfide bonds: #status experimental
F:9-10/Cross-link: cyclopeptide (Cys-Arg) #status experimental

Query Match 74.8%; Score 86; DB 2; Length 18;
Best Local Similarity 86.7%; Pred. No. 0.0002;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 4 RCICTRGFCRCICGR 18
DB 1 RCICTRGFCRCICGR 15

RESULT 2
A59089
theta defensin 1a precursor - rhesus macaque
C:Species: Macaca mulatta (rhesus macaque)
C:Date: 29-Oct-1999 #sequence #revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: A59089
R:Tang, Y.Q.; Yuan, J.; Osapay, G.; Osapay, K.; Tran, D.; Miller, C.J.; Ouellette, A.J.;
Science 286, 498-502, 1999
A:Title: A cyclic antimicrobial peptide produced in primate leukocytes by the ligation of
A:Reference number: A59089; MUID:99453140; PMID:10521339
A:Accession: A59089
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-76 <TRNA>
A:Cross-references: UNIPROT:P82270; GB:AF191100; NID:66137227; PIDN:AF04389.1; PID:66137227
C:Comment: For the complete mature sequence, see PIR:CS9089.
C:Superfamily: mammalian defensin
C:Keywords: antibacterial; antibiotic; antifungal; leukocyte; protein splicing
F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-64/Domain: amino-terminal propeptide #status predicted <PRO>
F:74-76/Domain: carboxyl-terminal propeptide #status predicted <CTR>

Query Match 55.7%; Score 64; DB 2; Length 76;
Best Local Similarity 83.3%; Pred. No. 0.23;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RCICTRGFCRCI 15
DB 65 RCICTRGFCRL 76

RESULT 3

E71602
probable integral membrane protein PFB0950W - malaria parasite (Plasmodium falciparum)

C/Species: Plasmodium falciparum
C/Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C/Accession: E71602

R:Gardner, M.J.; Tectel, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
Pereira, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998

A/Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A/Reference number: A71600; MUID:99021743; PMID:9804551

A/Accession: E71602

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-248 <GAR>

A/Cross-references: UNIPROT:Q96282; GB:AE001428; GB:AE001362; NID:93845316; PIDN:AACT197

A/Experimental source: clone 3D7

C/Genetics:

A/Genes: PFB0950W

Query Match 50.0%; Score 57.5; DB 2; Length 248;
Best Local Similarity 66.7%; Pred. No. 3;
Matches 10; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

QY 2 ICRCICTRGFCRCIC 16
DB 162 ICSCICT---CTCIC 173

RESULT 4

T24272

hypothetical protein T01B7.8 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T24272

R:Stim, M.
submitted to the EMBL Data Library, October 1995

A/Reference number: Z19867

A/Accession: T24272

A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: DNA

A/Residues: 1-164 <WTL>

A/Cross-references: UNIPROT:Q22048; EMBL:Z66499; PIDN:CAA91301.1; GSPDB:GN00020; CESP:TC

A/Experimental source: clone T01B7

C/Genetics:

A/Genes: CESP:T01B7.8

A/Map position: 2

A/Introns: 20/3; 90/2

Query Match 44.3%; Score 51; DB 2; Length 164;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GICRCICTRGFCRCICGR 18
DB 80 GCGCGCCCRPRCCCCRR 97

RESULT 5

T15651
hypothetical protein C27A2.5 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T15651

R:Nhan, M.

submitted to the EMBL Data Library, May 1996

A/Description: The sequence of C. elegans cosmid C27A2.

A/Reference number: Z18382

A/Accession: T15651

A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: DNA

A/Residues: 1-188 <NHA>

A/Cross-references: UNIPROT:Q18238; EMBL:U58760; NID:G1330384; PID:G1330389; PIDN:AA0071

A/Experimental source: strain Bristol NZ; clone C27A2

C/Genetics:

A/Genes: CESP:C27A2.5

A/Map position: 2

A/Introns: 19/3; 91/2

Query Match 44.3%; Score 51; DB 2; Length 188;
Best Local Similarity 50.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GICRCICTRGFCRCICGR 18
DB 81 GCGCGCCCRPRCCCCRR 98

RESULT 6

S32834
methylviologen-reducing hydrogenase chain vhcG [similarity] - Methanococcus voltae

C/Species: Methanococcus voltae

C/Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004

C/Accession: S32834; S16726

R:Klein, A.
submitted to the EMBL Data Library, August 1991

A/Reference number: S32833

A/Accession: S32834

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-306 <KLE>

A/Cross-references: UNIPROT:Q00406; EMBL:X61203; NID:9296614; PIDN:CAA43505.1; PID:929661

R:Halboth, S.; Klein, A.
submitted to the EMBL Data Library, August 1991

A/Description: Methanococcus voltae harbors two gene groups each of homologous (Nife) - ar

A/Reference number: S16721

A/Accession: S16726

A/Molecule type: DNA

A/Residues: 1-99, 'TA', 102-107, 'P', 126, 'LH', 129-306 <HAL>

A/Cross-references: EMBL:X61203

A/Note: the sequence is revised in Genbank entry X61203, release 117, (PIDN:CAA43505.1)

R:Halboth, S.; Klein, A.

Mol. Gen. Genet. 233, 217-224, 1992

A/Title: Methanococcus voltae harbors four gene clusters potentially encoding two (Nife)

A/Reference number: A59304; MUID:92293118; PMID:1603063

A/Contents: annotation

C/Genetics:

A/Genes: vhcG

C/Superfamily: methyl viologen-reducing hydrogenase gamma chain

Query Match 44.3%; Score 51; DB 2; Length 306;
Best Local Similarity 46.7%; Pred. No. 21;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 ICRCICTRGFCRCIC 16
DB 214 VCMGVATRASCRFC 228

RESULT 7

S58870
reelin precursor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 21-Jul-2003

C:Accession: S58870; S71844; I49297
R.D:Arcangelo, G.; Miao, G.G.; Chen, S.C.; Soares, H.D.; Morgan, J.I.; Curran, T.
Nature 374, 719-723, 1995
A>Title: A protein related to extracellular matrix proteins deleted in the mouse mutant
A:Reference number: I49297; MUID:95231649; PMID:7715726
A:Accession: S58870
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-3461 <DAR>
A:Cross-references: EMBL:U24703; NID:G902486; PID:G902487
R.D:Arcangelo, G.
submitted to the EMBL Data Library, April 1995
A:Reference number: S71844
A:Accession: S71844
A:Molecule type: mRNA
A:Residues: 1-215, 'T', 217-1905, 'S', 1907-3355, 'V', 3357-3391, 'N', 3393-3461 <DA2>
A:Cross-references: EMBL:U24703; NID:G902486; PID:G902487
F.1-77/Domain: signal sequence #status predicted <Sig>
F.128-3461/Product: reelin #status predicted <MAT>
F.1769-1795/Domain: EGF homology <EGF>

Query Match 43.9%; Score 50.5; DB 2; Length 3461;
Beet Local Similarity 52.6%; Pred. No. 1.3e+02;
Matches 10; Conservative 1; Mismatches 5; Indels 3; Gaps 1;

OY 1 GIC--RCICRGFCRCIC 16
Db 1777 GICDSGRVCVCDRGFGGFC 1795

RESULT 8

JCS677
RNA4 protein - Beet necrotic yellow vein mosaic virus
C:Species: Beet necrotic yellow vein mosaic virus
C:Date: 11-Nov-1997 #sequence_revision 11-Nov-1997 #text_change 09-Jul-2004
C:Accession: JCS677
R:Yu, J.L.; Han, C.G.; Yan, L.L.; Li, D.W.; Liu, Y.
Acta Microbiol. Sin. 37, 7-14, 1997
A>Title: cDNA cloning, sequence analysis and expression of RNA4 from beet necrotic yellow vein
A:Reference number: JCS677
A:Accession: JCS677
A:Molecule type: mRNA
A:Residues: 1-282 <YUA>
A:Cross-references: UNIPROT:O65670

Query Match 43.0%; Score 49.5; DB 2; Length 282;
Beet Local Similarity 42.1%; Pred. No. 30;
Matches 8; Conservative 1; Mismatches 5; Indels 5; Gaps 1;

OY 5 CICTRGFC----RCICGR 18
Db 183 CVCSCGVCYFNDNHCFCGR 201

RESULT 9

TIMB
trypsin inhibitor (Bowman-Birk) - mung bean
C:Species: Vigna radiata (mung bean)
C:Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
C:Accession: A01301
R:Zhang, Y.; Luo, S.; Tan, F.; Qi, Z.; Xu, L.; Zhang, A.
Sci. Sin. 25, 268-277, 1982
A>Title: Complete amino acid sequence of mung bean trypsin inhibitor.
A:Reference number: A01301
A:Accession: A01301
A:Molecule type: protein
A:Residues: 1-72 <ZHA>
A:Cross-references: UNIPROT:P01062
A>Note: three isoinhibitors are also found whose amino ends differ slightly from that of
A:Live-1, respectively
C:Comment: This inhibitor stoichiometrically inhibits trypsin in a molar ratio of 1:2.
C:Subfamily: Bowman-Birk proteinase inhibitor, Bowman-Birk inhibitor repeat homology
C:Keywords: duplication; serine proteinase inhibitor

```

F.11-39/Domin Bowman-Birk inhibitor repeat homology <BB1>
F.40-65/Domin Bowman-Birk inhibitor repeat homology <BB2>
F.112-66,13-28,18-62,18-26,36-43,40-55,45-53/Distalide bonds: #status predicted
F.120/inhibitory site: Lys (trypsin) #status predicted
F.147/inhibitory site: Arg (trypsin) #status predicted

Query Match          42.6%; Score 49; DB 1; Length 72;
Best Local Similarity 58.8%; Pred. No. 13;
Matches 10; Conservative 2; Mismatches 1; Indels 4; Gaps 2;

QY      3 CR-CICTR---GFCRCI 15
         |||:|||||
DB       40 CKSCICTRSMPEKCRCL 56

RESULT 10
JC1066
C.Species: Vigna radiata (mung bean)
C.Date: 02-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 18-Aug-2000
C.Accession: JCI066
R.Chen, C.Q.; Mao, J.F.; Zhang, M.F.; Dai, J.F.
Chinese J. Biotechnol. 9, 54-60, 1993
A.Title: Synthesis of mung bean trypsin inhibitor by the combination of the single strand
A.Reference number: JCI066
A.Accession: JCI066
A.Molecule type: DNA
A.Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
C.Keywords: serine proteinase inhibitor
F.11-40/Domin Bowman-Birk inhibitor repeat homology <BB1>
F.14-66/Domin Bowman-Birk inhibitor repeat homology <BB12>

Query Match          42.6%; Score 49; DB 2; Length 73;
Best Local Similarity 58.8%; Pred. No. 14;
Matches 10; Conservative 2; Mismatches 1; Indels 4; Gaps 2;

QY      3 CR-CICTR---GFCRCI 15
         |||:|||||
DB       41 CKSCICTRSMPEKCRCL 57

RESULT 11
S08167
Balbiani ring 3 protein - midge (Chironomus tentans)
C.Species: Chironomus tentans
C.Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Aug-2004
C.Accession: S08167
R.Paulsson, G.; Lendahl, U.; Galli, J.; Ericsson, C.; Wieslander, L.
J. Mol. Biol. 211, 331-349, 1990
A>Title: The balbiani ring 3 gene in Chironomus tentans has a diverged repetitive structure
A.Reference number: S08167; MUID:90172404; PMID:1689777
A.Accession: S08167
A.Status: not compared with conceptual translation
A.Molecule type: DNA
A.Residues: 1-1700 <PAU>
A.Cross-references: UNIPROT:Q03376; GB:X52263; NID:g7057; PIDN:CA36506.1; PID:g7058
C.Genetics:
A.Gene: BR3
A.Map position: 4

Query Match          42.6%; Score 49; DB 2; Length 1700;
Best Local Similarity 23.3%; Pred. No. 1,2e+02;
Matches 7; Conservative 4; Mismatches 3; Indels 16; Gaps 1;

QY      3 CRCICRG-----FCGCIC 16
         |||::|:
DB       1245 CRCVCPKNMEKPADNCKTKMNDMDMCQCVC 1274

RESULT 12
T22945
```

hypothetical protein T01D3.1 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T22945; T24295

R/Percy, C.

submitted to the EMBL Data Library, October 1996

A/Reference number: Z19640

A/Accession: T22945

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-3191 <WIL>

A/Cross-references: UNIPROT:O01335; EMBL:Z81094; PIDN:CA803155.1; GSPDB:GN00023; CESP:T0

A/Experimental source: clone F58G11

R/Steward, C.

submitted to the EMBL Data Library, October 1996

A/Reference number: Z19870

A/Accession: T24295

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-3191 <W12>

A/Cross-references: EMBL:Z81110; PIDN:CA803261.1; GSPDB:GN00023; CESP:T01D3.1

A/Experimental source: clone T01D3

C/Genetics:

A/Gene: CESP:T01D3.1

A/Map position: 5

A/Introns: 18/1; 73/2; 101/3; 241/2; 251/1; 327/3; 383/3; 455/3; 494/1; 793/1; 905/3; 10

Query Match 42.6%; Score 49; DB 2; Length 3191;

Best Local Similarity 30.6%; Pred. No. 1.8e+02;

Matches 11; Conservative 2; Mismatches 1; Indels 22; Gaps 2;

Qy 1 GICRC-----ICTR-GFCRC 14

Db 1182 GLCKCEGMOGSRQRCPLCNSCLNGICTRPFSC 1217

RESULT 13

S07405

protease inhibitor (Bowman-Birk) C-II - soybean

C/Species: Glycine max (soybean)

C/Date: 02-Dec-1993 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C/Accession: S07405; S29608; S40113

R/Joudrier, P.E.; Foard, D.B.; Floener, L.A.; Larkins, B.A.

Plant Mol. Biol. 10, 35-42, 1987

A/Title: Isolation and sequence of cDNA encoding the soybean protease inhibitors PI IV a

A/Reference number: S07405

A/Accession: S07405

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-83 <JOU>

A/Cross-references: UNIPROT:P01063; EMBL:M20732; NID:G169944; PIDN:AAA33953.1; PID:G1699

A/Note: the sequences of codons 8-13 and 14-27 are interchanged in the authors' translat

R/Bek, J.M.; Kim, S.I.

submitted to the EMBL Data Library, October 1992

A/Description: Nucleotide sequence of a cDNA encoding the soybean Bowman-Birk proteinase

A/Reference number: S29559

A/Accession: S29608

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-83 <BAE>

A/Cross-references: EMBL:X68705; NID:G18567; PIDN:CAA48656.1; PID:G18568

R/Giordano, A.; Delladonne, M.; Fogher, C.; Marchetti, S.

submitted to the EMBL Data Library, December 1993

A/Description: Nucleotide sequence encoding a soybean C-II proteinase inhibitor.

A/Reference number: S40113

A/Accession: S40113

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-83 <GIO>

A/Cross-references: EMBL:X76727; NID:G436413; PIDN:CAA54144.1; PID:G436414

C/Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology

C/Keywords: serine proteinase inhibitor

F/22-48/Domain: Bowman-Birk inhibitor repeat homology <BB1>

F/49-74/Domain: Bowman-Birk inhibitor repeat homology <BB12>

Query Match 42.2%; Score 48.5; DB 2; Length 83;

Best Local Similarity 60.0%; Pred. No. 17;

Matches 9; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

Qy 4 RCICTR--GFCRCI 15

Db 51 RCACTRSMFGQCRCL 65

RESULT 14

JC2225

Bowman-Birk proteinase Isoinhibitor C-II precursor (clone pB24) - soybean

C/Species: Glycine max (soybean)

C/Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 18-Aug-2000

C/Accession: JC2225

R/Bek, J.M.; Song, J.C.; Choi, Y.D.; Kim, S.I.

Bioescl. Biotechnol. Biochem. 58, 843-846, 1994

A/Title: Nucleotide sequence homology of cDNAs encoding soybean Bowman-Birk type proteinase

A/Reference number: JC2224; MUID:94289861; PMID:7764974

A/Accession: JC2225

A/Molecule type: mRNA

A/Residues: 1-94 <BAE>

A/Comment: This protein regulates endogenous proteinase during germination, stores sulfa

C/Genetics:

A/Start codon: GTT

C/Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology

C/Keywords: duplication; seed; serine proteinase inhibitor

F/1-18/Domain: signal sequence #status predicted <SIG>

F/19-94/Product: Bowman-Birk proteinase Isoinhibitor C-II #status predicted <MAT>

F/33-59/Domain: Bowman-Birk inhibitor repeat homology <BB1>

F/60-85/Domain: Bowman-Birk inhibitor repeat homology <BB12>

Query Match 42.2%; Score 48.5; DB 2; Length 94;

Best Local Similarity 60.0%; Pred. No. 18;

Matches 9; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

Qy 4 RCICTR--GFCRCI 15

Db 62 RCACTRSMFGQCRCL 76

RESULT 15

TISYC2

protease inhibitor (Bowman-Birk) C-II precursor - soybean

C/Species: Glycine max (soybean)

C/Date: 24-Apr-1984 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C/Accession: A22636; A01302

R/Hammond, R.W.; Foard, D.B.; Larkins, B.A.

J. Biol. Chem. 259, 9883-9890, 1984

A/Title: Molecular cloning and analysis of a gene coding for the Bowman-Birk protease int

A/Reference number: A92489; MUID:84264652; PMID:6086657

A/Contents: annotation

A/Note: the sequence has been revised in reference A92540

R/Hammond, R.W.; Foard, D.B.; Larkins, B.A.

J. Biol. Chem. 260, 7806, 1985

A/Reference number: A92540

A/Contents: erratum

A/Accession: A22636

A/Molecule type: DNA

A/Residues: 1-103 <HAM>

A/Cross-references: UNIPROT:P01063; GB:X01967; NID:G169942; PIDN:AAA33952.1; PID:G169943

R/Ogami, S.; Ikenaka, T.

J. Biochem. 82, 1523-1531, 1977

A/Title: Studies on soybean trypsin inhibitors. XI. Complete amino acid sequence of a soy

A/Reference number: A01302; MUID:78087480; PMID:599141

A/Accession: A01302

A/Molecule type: protein

A/Residues: 28-103 <ODA>

A/Comment: This protein inhibits trypsin, elastase, and chymotrypsin. The site of interac

C/Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology

C/Keywords: duplication; seed; serine proteinase inhibitor

F/1-27/Domain: signal sequence #status predicted <SIG>
F/28-103/Product: proteinase inhibitor (Bowman-Birk) C-II #status experimental <MAT>
F/42-68/Domain: Bowman-Birk inhibitor repeat homology <BB1>
F/59-94/Domain: Bowman-Birk inhibitor repeat homology <BB2>
F/41-95,42-57,45-91,47-55,65-72,69-84,74-82/Disulfide bonds: #status predicted
F/49/Inhibitory site: Ala (elastase) #status predicted
F/76/Inhibitory site: Arg (trypsin) #status experimental

Query Match 42.2% Score 48.5; DB 1; Length 103;
Best Local Similarity 60.0%; Pred. No. 20;
Matches 9; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

Qy 4 RCICTR---GFCRCI 15
Db 71 RCACTRSMPCQCRCL 85

Search completed: March 22, 2005, 20:50:38
Job time : 48 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 22, 2005, 20:23:06 ; Search time 173 Seconds

(Without alignments)
53.280 Million cell updates/sec

Title: US-10-721-839-32

Sequence: 1 GICRCICTRGRCRCICGR 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 segs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seg length: 0

Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	64	55.7	76	1	TDIA_MACMU	P82270 macaca mula
2	61.5	53.5	168	2	087BL8	087b18 xylella fas
3	58.5	50.9	83	2	Q7PG24	Q7PG24 anopheles g
4	58	50.4	168	2	Q6P874	Q6P874 mus musculu
5	58	50.4	168	2	Q8CH20	Q8CH20 mus musculu
6	58	50.4	168	2	Q9D912	Q9D912 mus musculu
7	58	50.4	173	2	Q9DAK2	Q9DAK2 mus musculu
8	57.5	50.0	307	2	Q96282	Q96282 plasmodium
9	56.5	49.1	163	2	Q8VU20	Q8VU20 mycobacteri
10	55	47.8	146	2	Q7QB44	Q7QB44 anopheles g
11	54.5	47.8	183	2	Q7PRP5	Q7PRP5 anopheles g
12	54.5	47.4	190	2	Q9UI23	Q9UI23 homo sapien
13	54.5	47.4	307	2	Q9H9U3	Q9H9U3 homo sapien
14	54	47.0	193	2	Q8S6V3	Q8S6V3 cryza saviv
15	54	47.0	201	2	Q6Z0S2	Q6Z0S2 homo sapien
16	54	47.0	609	2	Q7QNX8	Q7QNX8 giardia lam
17	53.5	46.5	379	2	Q7SXV0	Q7SXV0 brachydanio
18	53	46.1	336	2	Q7PVN9	Q7PVN9 anopheles g
19	53	46.1	657	2	Q7OVH8	Q7OVH8 giardia lam
20	53	46.1	1365	2	Q7SN87	Q7SN87 homo sapien
21	53	46.1	2871	2	Q7SN87	Q7SN87 homo sapien
22	52.5	45.7	129	2	Q7PU70	Q7PU70 anopheles g
23	52.5	45.7	512	2	Q6RY99	Q6RY99 rattus norv
24	52.5	45.7	2809	1	FBN3_HUMAN	Q7SN90 homo sapien
25	52.5	45.7	3008	2	Q6O144	Q6O144 bos taurus
26	52	45.2	112	2	Q9U745	Q9U745 tenebrio mo
27	52	45.2	274	2	Q94961	Q94961 cryza saviv
28	52	45.2	848	2	Q93U55	Q93U55 carsonella
29	51.5	44.8	101	2	Q7YUJ2	Q7YUJ2 trypanosoma
30	51.5	44.8	118	2	Q8C9N2	Q8C9N2 mus musculu
31	51.5	44.8	131	2	Q9D261	Q9D261 mus musculu

32	51.5	44.8	160	2	Q9H654	Q9H654 homo sapien
33	51.5	44.8	243	2	Q6ZMP3	Q6ZMP3 homo sapien
34	51.5	44.8	462	2	Q6GQP2	Q6GQP2 brachydanio
35	51	44.3	82	2	Q7PKA1	Q7PKA1 anopheles g
36	51	44.3	142	2	Q8NA00	Q8NA00 homo sapien
37	51	44.3	164	2	Q22048	Q22048 caenorhabdi
38	51	44.3	166	2	Q95QY1	Q95QY1 caenorhabdi
39	51	44.3	188	2	Q18238	Q18238 caenorhabdi
40	51	44.3	197	2	Q17641	Q17641 caenorhabdi
41	51	44.3	306	1	VHCG_METVO	Q00406 methanococc
42	51	44.3	602	2	Q7SNZ5	Q7SNZ5 chlamydomon
43	51	44.3	937	2	Q9BLJ1	Q9BLJ1 clona intes
44	51	44.3	4539	1	LRIB_MOUSE	Q9J118 mus musculu
45	50.5	43.9	94	2	Q8C0H3	Q8C0H3 mus musculu

ALIGNMENTS

RESULT 1
ID TDIA_MACMU STANDARD; PRT; 76 AA.
AC P82270; Q9TU01;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Theta defensin-1, subunit A precursor (RTP-1a) (Demi-defensin 2).
GN Name=RTDIA;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 65-73, TISSUE SPECIFICITY,
RP DEVELOPMENTAL STAGE, AND DISULFIDE BONDS.
RC TISSUE=Bone marrow, and Leukocyte;
RX MEDLINE=99453140; PubMed=10521339; DOI=10.1126/science.286.5439.498;
RA Tang Y.-Q., Yuan J., Oesabay G., Oesabay K., Tran D., Miller C.J.,
RA Ouellette A.J., Seistad M.E.;
RT "A cyclic antimicrobial peptide produced in primate leukocytes by the
RT ligation of two truncated alpha-defensins.";
RL Science 286:498-502 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Zhao C., Nguyen T., Lehrer R.I.;
RT "CDNA cloning of three alpha-defensins and three demidefensins from
RT rhesus monkey bone marrow.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Active against the Gram-positive bacteria *S. aureus* and
CC *L. monocytogenes*, Gram-negative bacteria *S. typhimurium* and *E. coli*
CC M135 and fungi *C. albicans* and *C. neoformans* in vitro.
CC -!- SUBUNIT: Forms a cyclic heterodimer composed of subunits A and B;
CC disulfide-linked.
CC -!- TISSUE SPECIFICITY: Expressed in bone marrow. Detected in
CC promyelocytes, myelocytes and mature neutrophils and monocytes.
CC -!- DEVELOPMENTAL STAGE: Expression begins early during granulocyte
CC myelopoiesis.
CC -!- PTM: This is a cyclic peptide.
CC -!- SIMILARITY: Belongs to the corticostatin/defensin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF191100; AAF04389.1; -;
CC EMBL: AF191102; AAF04391.1; -;
CC EMBL: AF184157; AAF07924.1; -;

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DR  PIR; A59089; A59089.
DR  InterPro; IPR002366; Defensin_propep.
DR  Pfam; PF00879; Defensin_propep; 1.
DR  PROSITE; PS00269; DEFENSIN; FALSE NEG.
KW  Antibiotic; Defensin; Direct protein sequencing; Fungicide; Signal.
FT  SIGNAL 1 22 Potential.
FT  PROPEP 23 64
FT  PEPTIDE 65 73 Theta defensin-1, subunit A.
FT  PROPEP 74 76
FT  DISULFID 66 66 Interchain (with C-66 of subunit B).
FT  DISULFID 68 73
FT  CONFLICT 38 38
SQ  SEQUENCE 76 AA; 8242 MW; BE207932A030590 CRC64;

Query Match 55.7%; Score 64; DB 1; Length 76;
Best Local Similarity 83.3%; Pred. No. 0.47;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RCICITRGFCRCICR 15
DB 65 RCICITRGFCRRL 76

RESULT 2
Q87BL8 PRELIMINARY; PRT; 168 AA.
AC Q87BL8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=PD1431;
OS Xylella fastidiosa (strain Temecual / ATCC 700964).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=183190;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22421331; PubMed=12533478;
RX DOI=10.1128/JB.185.3.1018-1026.2003;
RA Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
RA Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,
RA Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,
RA Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorri H., Tsai S.M.,
RA Carier H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
RA Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.B.,
RA Martino C.L., Gaglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
RA Baia G.S., Bianco S.R., Brito M.S., Camavan F.S., Celestino A.V.,
RA da Cunha A.F., Penille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
RA Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sasaki F.T., Sena J.A.D.,
RA de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zartos L.G.,
RA Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
RA Kitajima J.P.;
RT "Comparative analyses of the complete genome sequences of Pierce's
RT disease and citrus variegated chlorosis strains of Xylella
RT fastidiosa."
RL J. Bacteriol. 185:1018-1026 (2003).
DR EMBL; AE012558; AAO29277.1; -.
KW Complete proteome.
SQ SEQUENCE 168 AA; 17967 MW; 87A25F3C5E816C8 CRC64;

Query Match 53.5%; Score 61.5; DB 2; Length 160;
Best Local Similarity 50.0%; Pred. No. 1.8;
Matches 9; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY 1 GICRCITRGFCRCICR 18
DB 144 GVCCTCCVCG---CVCQG 158

RESULT 3
Q7PG24 PRELIMINARY; PRT; 83 AA.

```

```

AC Q7PG24;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP00000023115.
GN Name=ENSANG00000021478;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -1 CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008846; EAA45095.1; -.
SQ SEQUENCE 83 AA; 9462 MW; 7F4B67437A0B5EB4 CRC64;

Query Match 50.9%; Score 58.5; DB 2; Length 83;
Best Local Similarity 47.1%; Pred. No. 2.5;
Matches 8; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY 2 ICRCITRGFCRCICR 18
DB 69 VCVVCV---CMVCVGR 82

RESULT 4
Q6P8T4 PRELIMINARY; PRT; 168 AA.
AC Q6P8T4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE 4931420D14R1k protein.
GN Name=4931420D14R1k;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheifter C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.U., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallari S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherck A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Director MGC Project;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC061079; AAH61079.1; -.

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SQ SEQUENCE 168 AA; 18947 MW; B00FD3D27B9BF768 CRC64;
Query Match 50.4%; Score 58; DB 2; Length 168;
Best Local Similarity 56.2%; Pred. No. 5.1;
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 3 CRCTCTRGFCRCICGR 18
DB 66 CRCCCYCRCCRCRCCSR 81

RESULT 5
O8CH20 PRELIMINARY; PRT; 168 AA.
AC O8CH20;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Basic protein CKTIR3.
GN Name=4931420D1AR1k; Synonyms=CktIr3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
[3]
RP SEQUENCE FROM N.A.
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RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
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RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
[3]
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RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
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RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
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RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
[3]
RP SEQUENCE FROM N.A.
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RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
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RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
[3]
RP SEQUENCE FROM N.A.
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RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
[3]
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RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
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RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=992792
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RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The RANTOM Consortium,
RA "the RIKEN Genome Exploration Research Group Phase I & II Team";
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.153600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Saeki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitenuma T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsubiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Hanagaki T., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Koijima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Masuyama T., Miyazaki A., Nishi K., Nomura K., Numasaki R., Ono M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Soabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Mutamatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK006892; BAB24782.1; -
DR GGD; MG1:1913992; AB3142014.RK.
KW Hypothetical protein.
SQ
SEQUENCE 168 AA; 18931 MW; 7A2BD279612A5E94 CRC64;

Query Match 50.4%; Score 58; DB 2; Length 168;
Best Local Similarity 56.2%; Pred. No. 5.1;
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

DY 3 CRCTCTGFCFCTCGR 18
||| ||| |
Db 66 CRCCCHCRCCGCCSR 81

RESULT 7
Q9D4K2 PRELIMINARY; PRT; 173 AA.

ID Q9D4K2
AC Q9D4K2;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone#431420D14 product:hypothetical cysteine-rich region
DE containing protein, full insert sequence.
OS Name=431420D14.RK;
GS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;

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RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA "RIKEN FANTOM Consortium";
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN (3)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium;
RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN (4)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subcloning of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN (5)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoke S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Iehi Y., Nakamura S., Hazama M., Nishire T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujitake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-Format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN (6)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoaka T., Hori F.,
RA Imocani K., Iehi Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki K., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toyota T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK016467; BAB30253.1;
DR MGD; MGI:1913992; 4931420D1Arik.
KW Hypothetical protein.
SQ SEQUENCE 173 AA; 19581 MW; 147B6F155AC29PDF CRC64;

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Query Match 50.4%; Score 58; DB 2; Length 173;
Best Local Similarity 56.2%; Pred. No. 5.2;
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3 CRCTCTRGFCRCICGR 18
DB 66 CRCCCTCCRCRCRCSR 81

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RESULT 8
O96282 PRELIMINARY; PRT; 307 AA.
AC O96282;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein PFB0950W.
GN Name=PFB0950W;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=99021743; PubMed=9804551; DOI=10.1126/science.282.5391.1126;
RA Gardner M.J., Tettein H., Carucci D.J., Cummings L.M., Aravind L.,
RA Koonin E.V., Shallow S., Mason T., Yu K., Fujii C., Peterson J.,
RA Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Perera M.,
RA Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
RA Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
RT "Chromosome 2 sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Science 282:1126-1132(1998).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Pung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyte S.,
RA Chan M.-S., Nene V., Shallow S.J., Sub B., Peterson J., Angiuoli S.,
RA Perera M., Allen J., Selengut J., Haft D., Mather M.W., Valdivia A.B.,
RA Martin D.M.A., Fairhead A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrett B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
DR EMBL; AE001428; AAC71979.2;
DR PIR; E71602; E71602.
DR HSSP; P01056; I134.
DR INTERPRO; IPR001368; TNFR_C6.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 307 AA; 35537 MW; B95A3DB354D4BE71 CRC64;

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Query Match 50.0%; Score 57.5; DB 2; Length 307;
Best Local Similarity 66.7%; Pred. No. 9.6;
Matches 10; Conservative 0; Mismatches 2; Indels 3; Gaps 1;
QY 2 ICRCCTRGFCRCIC 16
DB 221 ICSCICT--CTCIC 232

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RESULT 9
O8VJ20 PRELIMINARY; PRT; 163 AA.
AC O8VJ20;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical protein.
GN OrderdilocusNames=MT3454;
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterinae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;

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RX DOI=10.1128/JB.184.19.5479-5490.2002;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.D., Deboy R.T., Dodson J.J., Gwinn M.L., Haft D.H.,
RA Hickey E.K., Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
RA Salzberg S.L., Delcher A., Deterback T.R., Feldman J.F., Kouri H.M.,
RA Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
RA Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL J. Bacteriol. 184:5479-5490(2002).
DR EMBL: AE000516; AAK4795.1; -.
DR TIGR: MT3454; -.
KM Hypochemical protein.
SQ SEQUENCE 163 AA; 18621 MW; B5E62AB951B2AC3C CRC64;

Query Match 49.1%; Score 56.5; DB 2; Length 163;
Best Local Similarity 60.0%; Pred. No. 7.6;
Matches 9; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Qy 3 CRCICTR-GFCRCIC 16
Db 137 CRHVCTRSYCRVLC 151

RESULT 10
Q7QBVA PRELIMINARY; PRT; 146 AA.
AC Q7QBVA;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AGCP1494 (Fragment).
GN Name=agcC47401; ORFNames=ENSANG000000012913;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RL Anopheles Genome Sequencing Consortium;
CC Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
DR EMBL: AAB01008859; EAA07639.1; -.
DR NON_TER 1
FT SEQUENCE 146 AA; 16746 MW; 7D32B8AABE776F98 CRC64;

Query Match 47.8%; Score 55; DB 2; Length 146;
Best Local Similarity 53.8%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CICTRGFCRCIC 17
Db 44 CVCVLGWCRCVCG 56

RESULT 11
Q7PRPS PRELIMINARY; PRT; 1823 AA.
AC Q7PRPS;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP00000019046 (Fragment).
GN Name=ENSANG00000016557;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
DR EMBL: AAB01008847; EAA06854.2; -.
DR HSSP; P00740; 1EDM.
DR InterPro: IPR00152; Asx_hydroxyl_5.
DR InterPro: IPR008985; ConA_like_1ec_g1.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR009030; Grow_fac_recept.
DR InterPro: IPR003410; Hyalin.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR001759; Pentaxin.
DR InterPro: IPR001211; PhospholipaseA2.
DR InterPro: IPR000436; Sushi_SCR_CCP.
DR InterPro: IPR002035; VWF_A.
DR Pfam: PF00008; EGF_5.
DR Pfam: PF02494; HVR_2.
DR Pfam: PF00354; Pentaxin; 1.
DR Pfam: PF00084; Sushi; 5.
DR Pfam: PF00092; VMA; 1.
DR PRINTS: PR00895; PENTAXIN.
DR PRINTS: PR00453; VWFADOMAIN.
DR Prodom: PD002153; Pentaxin; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_5.
DR PROSITE: PS0106; EGF_2; 4.
DR PROSITE: PS50026; EGF_3; 5.
DR PROSITE: PS50825; HVR_2.
DR PROSITE: PS50025; LAM_G_DOMAIN; 1.
DR PROSITE: PS00118; PA2_HIS; UNKNOWN_1.
DR PROSITE: PS50923; SUSI; 8.
DR PROSITE: PS50234; VWF; 1.
FT NON_TER 1
FT NON_TER 1823
FT SEQUENCE 1823 AA; 200582 MW; 5740C4C700804379 CRC64;

Query Match 47.8%; Score 55; DB 2; Length 1823;
Best Local Similarity 53.3%; Pred. No. 85;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ICRCICRGFCRCIC 16
Db 262 VCSCLTSGHYRCIC 276

RESULT 12
Q9UI23 PRELIMINARY; PRT; 190 AA.
AC Q9UI23;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE PRO0529.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Zhang C., Yu Y., Zhang S., Ouyang S., Luo L., Wei H., Zhou G.,
RA Zhang Y., Liu M., He F.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF11848; ARI16687.1; -.
SQ SEQUENCE 190 AA; 21480 MW; 4B8104A29AA33844 CRC64;

Query Match 47.4%; Score 54.5; DB 2; Length 190;
Best Local Similarity 44.4%; Pred. No. 15;
Matches 8; Conservative 3; Mismatches 4; Indels 3; Gaps 1;

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Job time : 175 secs

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